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Perfect score:
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Gapop_60.0
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1093
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### Result No. Q O O Score Query Match 43.6 146759 243780 134308 162530 194023 194023 210617 224148 228405 184961 195066 1800 1429 1429 247196 218817 240009 246796 Length 1514 1560 152 1410 1429 В 10 AR076190 AR124103 E23385 AC039822 AX165175 BD124885 BD126291 BC039388 AC015914 AC021541 AC024201 AC016179 AC016179 AC029406 AC103501 AC129021 AC129021 AC129021 AC129021 RATISCKIN3 BC038491 RATISCKIN3 AC128095 E23384 AX880020 BD012208 BD158150 AK027590 AC011488 BD176607 AB007144 AK097643 AY335738 BC022165 AB022341 BD127287 AK074799 AR076189 AR124102 SUMMARIES AR076190 Sequence AR124103 Sequence E23385 DNA encodin AC073822 Mus muscu AX165175 Sequence ED124885 Primer fo EC039388 Homo sapi AC032341 Homo sapi ED12785 Primer fo ED12785 Primer fo ED12785 Primer fo ED12785 Primer fo AK074799 Homo sapi ED1278607 Method of AK074799 Homo sapi AC07144 Homo sapi AC097643 Homo sapi AR076189 Sequence E23384 DNA encodin AX88020 Sequence E23384 DNA encodin AX88020 Sequence ED012208 Novel gen E012810 Primer fo AK027590 Homo sapi AC021541 Homo sapi AC034201 Rattus no AC123021 Mus muscu AC013501 Rattus no AC123021 Mus muscu AC033491 Nis muscu AC033491 Rat S6 Kina BC033491 Rat S6 S00 AC1280395 Rattus no AC128035 Mouse DNA AC128035 Rattus no AC128035 Rattus no AC114704 Rattus no AC120292 Rattus no AC094643 Rattus no AJ006971 Rattus no BC062076 Rattus no AB010083 Rattus no AB0101083 Rattus no Description

## ALIGNMENTS

REFERENCE AUTHORS		SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AC114704/c	RESULT 1
1 (bases 1 to 218817) Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,	Eukaryota, Metazoa, Chordata, Craniáta, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.	Rattus norvegicus (Norway rat)	HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.	AC114704.4 GI:25138818	AC114704	Rattus norvegicus clone CH230-55A15, WORKING DRAFT SEQUENCE.	AC114704 218817 bp DNA linear HTG 20-NOV-2002		

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JOURNAL
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AL Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23265882.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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Rat Genome Sequencing Consortium.
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                                             122230 GTCCAGCCGGCGGTGTGAGCCGTGAGGAGATCGAGCGCGAGGTGAGCATCCTGCGCGA 122171
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438 GATCCGCCACCCCAACATCATCACGCTGCACGATGTGTTCGAGAACAAGACAGATGTGGT 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 CCCTCAGCACGGGATTAACCTCACTTGACTGTTCTTGGGTCCCCGGGTGCCGGGCCAGCGT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 218817: contig of 218817 bp in length.
Location/qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                       GTCTGCAGCGCTTAGCTGTTCCTTCCCCCACAGCGGCCAGTTCGCCATCGTGCGCAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTCTCCCTCAAGGCAATCCCCAAGTGTCTGTCATGAGGCTCTTTGGGCAGTTCTGTTGT 122411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCTCTCCAAGGCAATCCCCAAGTGTCTGTCATGAGGCTCTTTGGGCAGTTCTGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
                                                                                              GTCCAGCCGCGCGCGTGAGCCCGTGAGGAGATCGAGCCGAGGTGAGCATCCTGCGCGA
                                                                                                                                                      CCAGCAGAAGGGCACCGGCATGGAGTACGCGGCCAAGTTCATAAAGAAGCGGCGCCTGCC
                                                                                                                                                                                                    CCAGCAGAAGGGCACCGGCATGGAGTACGCGGCCAAGTTCATAAAGAAGCGGCGCCTGCC
                                                                                                                                                                                                                                                                                                                                                        TGTGGGAAACCTGGGAACAGATGCACAGAGGCTGGGGTACAGAGTCCTGCCTTCCTCTGG
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Center clone name: CH230-55A15

Center clone name: CH230-55A15

Center clone name: CH230-55A15

Assembly program: Phrap; version 0.990329

Consensus quality: 207315 bases at least Q40

Consensus quality: 209091 bases at least Q20

Consensus quality: 209091 bases at least Q20

Consensus quality: 209091 bases at least Q20

Estimated insert size: 213462; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Contact: hgsc-help@bcm.tmc.edu
-----Project Information
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217464. .217908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-55A15"
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                                      Biswald, K. Bellat, J. Bellater, W., Calegron, E., Cardenas, V., Carter, K. (Cavazos, I., Ceass, H., Center, A., Chu, J., Chacko, J., Chaves, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., Divo, K., Calegra, M., Carder, M., Chen, Y., Chen, Z., Chu, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Chen, G., Chen, R., Cardy, M., Cree, A., Divo, K., Egen, A., Barch, G., C., Pearls, C., Pearls, G., Chen, R., Chen, Y., Chen, J., Chen, G., Chen, R., Falls, T., Fan, G., Chen, R., Falls, T., Fan, G., Chen, R., Falls, T., Fan, G., Chen, R., Falls, T., Faser, M., Guerar, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Guevara, M., Gebregorgis, E., Geer, K., Gill, R., Garcia, A., Garner, T., Guevara, M., Gunarathe, P., Haland, W., Hamilton, C., Hamilton, K., Hamilton, K., Harryey, Y., Halak, P., Hawes, A., Henderson, M., Hernandez, J., Kang, L., Kowar, C., Kast, C., Kelly, S., K
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Rattus norvegicus
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                                Direct Submission
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                 complement (222684. .223551)
/note="clone_boundary
clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-239B15"
                                                                                                                                             clone_end
                                                                                                                                                       /note="clone_boundary
clone end:T7
                                                                                                                                                                                                              end_sequence:BZ106119"
complement(222705. .223551)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Rattus norvegicus"
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                                                                                      sequence:BZ106119'
Score 477;
DB 2;
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of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 15, 2002 this sequence version replaced gi:23609710.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One
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Center project name: GWXC
Center clone name: CH220-239B15
Center clone name: CH220-239B15
Center clone name: CH220-239B15
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 207207 bases at least Q40
Consensus quality: 208683 bases at least Q20
Consensus quality: 208683 bases at least Q20
Consensus quality: 209684 bases at least Q20
Estimated insert size: 213125; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation Web site: http://www.hgsc.bcm.tmc.edu/ Contact: hgsc-help@bcm.tmc.edu ------Project Information

It currently the piece.

Length 240009;

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Allen, C., Allen, H., Alsbrooks, S., Adams, C., Alder, J.,
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Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
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Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Johnson, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC094643.5 GI:30466413
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
Rattus norvegicus (Norway rat)
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Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindarrne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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Mankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
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Wilson, R., Wilson, R., Shen, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Glbbs, R.A.
Direct Suhmission
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced gi:24818455.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
Submitted (15-SEP-2001) Human Genome Sequencing
of Molecular and Human Genetics, Baylor College
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 246796)
Rat Genome Sequencing Consortium.
Direct Submission
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of Medicine,
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TITLE
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AUTHORS
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REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

Contact: ngsc-ucrystantion
Center project Information
Center project name: GBBW
Center clone name: CH230-5BL8
Center clone name: CH230-5BL8
Center clone name: CH230-5BL8
Center clone name: CH230-5BL8
Center clone name: Atlas;
Assembly program: Atlas;
Consensus quality: 27791 bases at least Q40
Consensus quality: 230373 bases at least Q30
Consensus quality: 23086 bases at least Q30
Consensus quality: 23086 bases at least Q20
Consensus quality: 23086 bases at least Q20
Consensus quality: 23086 bases at least Q30
Consensus quality: 23086 bases at least Q30 Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor Co College of Medicine

NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/senbank\_draft\_data.html).
NOTE: This is a "working draft" sequence. It currently consists of 3 contigs. The true order of the pieces

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DEFINITION
ACCESSION
VERSION
KEYWORDS
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Rattus norvegicus mRNA for
AJ006971
AJ006971.1 GI:3250894
DAP-like kinase; dlk gene.
                                                                         RNO6971
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complement(241125...24
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/note="clone_boundary
clone_end:Sp6
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-5B18"
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Rattus norvegicus
Rattus norvegicus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (15-JUN-1998)
Genetik, Romerstr. 164,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kogel,D., Plottner,O., Landsberg,G., Scheidtmann,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (22-JUN-1998) Kogel D., Un
Genetik, Romerstr. 164, 53117 Bonn,
Location/Qualifiers
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ACTITICGACTITCIGGCTGAGAAGGA-TCACTGACAGAGGATGAGGCCACGCAGTTCCT
                                                                                                                                        CGATGTGTTCGAGAACAAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGCGA
                                                                                                                                                                                                                           GATCGAGCGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCATCATCACGCTGCA
                                                                                                                                                                                                                                                                                       GATCGAGCGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACATCATCACGCTGCA 467
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/product="DAP-like kinase"
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/cell_type="rat
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Pred. No. 2e-193;
0; Mismatches
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Bonn, GERMANY
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n, GERMANY
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KEYWORDS
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MEDLINE
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Ugdin, T.B., Toshiyuki, S.,
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
Abramson, R.D., Millahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S. W.,
Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,
Sanchez, A., Whitling, M., Madan, A., Young, A.C., Shevchenko, Y.,
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Schmerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                473
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                                                                          USA
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.
Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (CDNA Library Arrayed by: The I.M.A.G.E. Consortium (CDNA Library Arrayed by: The I.M.A.G.E.)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland; Web site. http://web.site.
                                                                                                                                                                                                                                                                                Submitted (10-NOV-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                         12477932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A.
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MGC.
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CGATGTGTTCGAGAACAAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGCGA

527

407 293 467

GGCCAAGTTCATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGGGTGTGAGCCGTGAGGA
GATCGAGCGCGAGGTGAGCATCCTGCGGCGAGATCCGCCCAACATCATCATCACGCTGCA
GATCGAGCGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCATCACGCTGCA

348

GCCAAGTTCATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGCGGTGTGAGCCCGTGAGGA

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Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Blatrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

Dietrich, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,

Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J. C.,

McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Young, A., Zhang, L.-H. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be following the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 137 Row: h Column: 12 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 119681-Location/Qualifiers
                                                                                                                                                    Similarity
CAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGC 233
                                             CAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGC
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                  /note="S_TKC; Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine-specific kinase subfamily. The enzymatic activity of these protein kinases is controlled by phosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal autoregulatory tail".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRRREDGARKPERRRLRAARLREYSLKSHSSMPRNTSYASFERFSRVLEDVAAAEQGL
RELQRGRRQCRERVCALRVAAEQREARCRDGSAGLGRDLRRLRTELGRTEALRTRAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DFLAEKESLTEDEATOFLKQILDGVHYLHSKRIAHFDLKPENIMLLDKHAASPRIKLI
DFGIAHRIEAGSEFKNIFGTPEFVAPEIVNYEPLGLEADMWSIGVITYILLSGASPFL
GETKQETLTNISAVNYDFDEEYFSSTSELAKDFIRRLLVKDPKRRMTIAQSLEHSWIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="Death-associated like kinase"
/protein id="AAH62076.1"
/db_xref="GI:3304024"
/db_xref="LocusID:64391"
/tanslation="MSTFRQEDVEDHYEMGEELGSGQFAIVRKCQQKGTGMEYAAKFI
KKRRLPSSRRGVSREEIEREVSILREIRHPNIITLHDVFENKTDVVLILELVSGGELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    <u>EARAALLGAGGIKRRICRIENRYDALAAQVAAEVQFVRDIVRALEQERIQAECGVR'</u>
                                                                                                                                                                                                                                                                              db xref="CDD:cd00180"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:10116"
/clone="MGC:72441 IMAGE:5599435"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="Dapkl"
db_xref="LocusID:64391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CI CGAP Pr29, 39, 42"
Clone lib="NCI CGAP_Pr50"
lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="RGD:621766"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  tissue_type="Prostate, pool
CI CGAP Pr29, 39, 42"
                                                                                                                                                 34.1%;
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                                                                                                                       0;
                                                                                                                    Score 373; DB 10
Pred. No. 2e-193;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pCMV-SPORT6.1"
                                                                                                                                                                              DB 10; Length 1560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of NCI_CGAP_Pr30, 40,
                                                                                                                       0;
                                                                                                                       Indels
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                                                                                                                    Gaps
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ORGANISM
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AB010083
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                                                Query Match
Best Local S
Matches 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             707
                          648
                                                   119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB010083
AB010083. GI:3219221
AB010083. I. GI:3219221
PKH alpha; kinase domain of PKH alpha.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
13
                                                                                                                                                                                                                                                                                            Submitted (29-DEC-1997) Kiyomitsu Nara, Mitsubishi Kasei Institute of Life Sciences, Department of Glycobiology; Minamiloya 11, Machida, Tokyo 194, Japan (E-mail:nara@libra.ls.m-kagaku.co.jp, Tel:81-427-24-6316)
Tel:81-427-24-6316
                                                                                                                                                                                                                                                                                                                                                                                  A novel protein kinase, PKH alpha
hippocampus
Published Only in DataBase (1998)
2 (bases 1 to 152)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB010083 mRNA for PKH alpha, partial
                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                    Nara, K.
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCAGAGTTCGTCG 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGATGTGTTCGAGAACAAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCCGGCGGCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGACTTTGGCATCGCGCACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACTITICGACTITCIGGCIGAGAAGGAGTCACIGACAGAGGATGAGGCCACGCAGTICCI
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               GCCAGAGTTCGTCG
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  AAGCCGGAGAACATCATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 152)
                                                   Conservative
                                                                                                            /translation="HCDFKPENIMLLDKHAASPRIKLIDFGIAHRIEAGSEFKNIFGT
PAYFAP"
                                                                                                                                    /product="PKH alpha"
/protein_id="BAA28810.1"
/db_xref="GI:3219222"
                                                                                                                                                                                   /function="putative serin/threonine protein kinase"
/note="kinase domain of PKH alpha"
                                                                                                                                                                                                                         /tissue
                                                                                                                                                                                                                                               organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Wister ST"
                                                                                                                                                                          codon_start=1
                                                                                                                                                                                                                                     _xref="taxon:10116"
                                                            10.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              780
                                                                                                                                                                                                                        type="hippocampus"
                                                   0
                                                             Score 119;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                       PKH alpha,
                                                 red. No. 2e-53;
Mismatches
                                                                         DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                        expressed in
                                                   0;
                                                                        Length 152;
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ial cds.
                                                   Indels
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                            707
     72
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REFERENCE
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AB007143
LOCUS
DEFINITION
ACCESSION
VERSION
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AUTHORS
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SOURCE
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                                                                            LOCUS
DEFINITION
ACCESSION
                                                                                                               RESULT 8
AR076190
                                                    VERSION
KEYWORDS
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      REFERENCE
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JOURNAL
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Matches
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                            ORGANISM
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                                                                                                                                                                  196
                                                                                                                                                                                        415
                                                                                                                                                                                                                 44;
      Unclassified.
1 (bases 1 to 1429)
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73 GACTTTGGCATCGCGCACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCAC
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Mus musculus mRNA for ZIP-kinase,
AB007143
AB007143.1 GI:2911157
                                                                                                                                                               AR076190
Sequence
AR076190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (10-SEP-1997) Shizuo Akira, Hyogo College of Medicine, Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo 663, Japan (E-mailakira@hyo-med.ac.jp, Tel:+81-798-45-6357, Fax:+81-798-46-3164)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Xawai,T., Matsumoto,M., Takeda,K., Sanjo,H. and Akira,S.
ZIP kinase, a novel serine/threonine kinase which mediates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (house mouse)
Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Akira, S. and Kawai, T. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9488481
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                                                  Unknown.
                                                                                                                              AR076190.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.0%; Score 44; DB ilarity 100.0%; Pred. No. 3: Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="ZIP-kinase"
/prodein_id="ZIP-kinase"
/protein_id="BAR24954.1"
/protein_id="MaR24954.1"
/protein_id="MaR24954.1"
/db_xref="GI:2911154"
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/db_xref="GI:2911154"
/db_xref="GI:2911154"
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/protein_id="Mar24954.1"
/protein_id="Mar24954.1"
/protein_id="Mar249511154"
/protein_id="Mar24951154"
/protein_id="Mar24954"
/prote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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                                                                                                                                  GI:10002936
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                                                                                                                                                                                                     1429 bp
patent US 5958748.
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3.5e-12;
thes 0;
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complete
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                                                                                                                                                                                                                                                            PAT 30-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Patent: JP 199098984-A
SCIENCE & TBCH AGENCY
OS Unidentified
PN JP 199908984-A/2
PN 13-APR-1999
PF 26-SEP-1997 JP 199
PR SHIZUO SHINRA, TARO
PC C12N15/09, C12N1/21
PC (12N19), C12R1:19
Strandedness: Double;
CC Topology: Linear;
                                                                                                                                                                                                                                                                                                                                                                           196 CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 239
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                                                                                                                                                                                                                                       DNA encoding serine/threonine
E23385
E23385.1 GI:13024387
JP 199908984-A/2.
unidentified
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                                                                                                                                                          1 (bases 1 to 1429)
Shizuo,S. and Taro,K.
DNA encoding serine/threonine kinase
Patent: JP 1999098984-A 2 13-APR-1999;
                                                                                                                                                                                                                 unclassified
                                                                                                                                                                                                                               unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Akira, S. and Kawai, T.

DNA coding for serine/threonine kinase
Patent: US 6171841-A 4 09-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
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Sequence 4 from patent US 6171841.
AR124103
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                                        SHIZUO SHINRA, TARO KAWAI
C12N15/09, C12N1/21, C12N9/12//(C12N15/09, C12R1:91), (C12N1/21,
C12R1:19),
         (C12N9/12,C12R1:19),C12N15/00,(C12N15/00,C12R1:91)
                                                                                          13-APR-1999
26-SEP-1997 JP 1997261589
                                                                                                                     JP 1999098984-A/2
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/mol_type="unassigned DNA"
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S 5958748-A 4 28-SEP-1999;
Location/Qualifiers
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/mol_type="unassigned DNA"
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Pred. No.
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AC073822
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Best Local Similarity
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Consensus quality: 236727 bases at least Q40
Consensus quality: 244906 bases at least Q30
Consensus quality: 244906 bases at least Q30
Consensus quality: 244906 bases at least Q20
Estimated insert size: 243000; agarose-fp estimation
Quality coverage: 7.76 in Q20 bases; agarose-fp estimation
Quality coverage: 7.76 in Q20 bases; agarose-fp estimation
Quality coverage: 7.76 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a "working draft" sequence. It currently
* consists of 16 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* Provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 18948 19047: gap of unknown length
* 20570 20569: gap of unknown length
* 20570 27716: gap of unknown length
* 27717 27816: gap of unknown length
* 27817 29329: contig of 1513 bp in length
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Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 247196)
DOB Joint Genome Institute
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HTG; HTGS PHASE2; HTGS DRAFT.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center clone name: RPCI-23_85K13
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Center Project Name: 1769765
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DOE Joint Genome Institute.
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Mammalia; Eutheria; Rodentia;
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/db_xref="taxon:32644"
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Matches 44
         Query Match
Best Local S
Matches 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44;
         ch 2.4%; Score 26; DB 6; 1 Similarity 100.0%; Pred. No. 0.038; 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                        Shimkets,R.A. and Leach,M.
Nucleic acids containing single nucleotide
methods of use thereof
Patent: WC 0138586-A 370 31-MAY-2001;
Curagen Corporation (US)
                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                         AX165175
Sequence 370 from Patent
AX165175
AX165175.1 GI:14546004
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178102
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-85K13"
                                                                                                                                               /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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                                                                                                /note="single nucleotide polymorphism Accession number cg43919086"
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62574: gap of unknown length
66039: contig of 33045 bp in length
66039: gap of unknown length
66039: gap of unknown length
91228: contig of 25089 bp in length
91228: gap of unknown length
115460: contig of 24132 bp in length
13567: contig of 17007 bp in length
132667: gap of unknown length
132667: gap of unknown length
136289: gap of unknown length
136289: contig of 3522 bp in length
136289: contig of 4812 bp in length
1378101: contig of 4812 bp in length
178101: gap of unknown length
178201: gap of unknown length
187292: contig of 9091 bp in length
187392: gap of unknown length
18820: gap of unknown length
18820: gap of unknown length
193155: gap of unknown length
193155: gap of unknown length
20518: gap of unknown length
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WO0138586.
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                                                                     AUTHORS
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                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 757)

Ota, T., Nishikawa, T., Isogai, T., Hayashi, K., Ishii, S., Kawai, Y., Wakamatsu, A., Sugiyama, T., Nagai, K., Kojima, S., Otsuki, T. and
                                                                                                                                        Homo sapiens (human)
Koga, H.

Primer for synthesizing full-length cDNA
Patent: JP 2002017375-A 1722 22-JAN-2002;
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Вb S

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC C12
Primer
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                                                                                                                                                                                                                                             l Similarity
26; Conserv
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HELIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/316
PD 22-JAN-2002
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Primer for synthesizing full-length cDNA and use thereof. BD126291 BD126291. GI:23221236 JP 2002017375-A/1722.
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SHINICHI KOJIMA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JP 2002017375-A/316
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ner for synthesizing full-length cDNA and use thereof FH F
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
                                                                                                                                                                                                                                             2.4%; Score 26; DB
larity 100.0%; Pred. No. 0.0
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 /organism='Homo
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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OS Homo sapiens (human)
PN JP 2002017375-A/1722
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIKAWA, T
PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOY
SHINICHI KOJIMA,
PI TETSUUI OTSUKI, HISASHI KOGA
PC
CONTESON CONTOCOLORIO
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                                                                                                                                                                                                     Email: cgppbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI) &
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human of Center, Stanford University School of Medicine, Stanford, Center, Stanford University School of Medicine, Stanford, Meb site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                      Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAK Plate: 77 Row: C Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: Excellent library of origin.
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Homo sapiens, clone IMAGE:5298774,
EC039388
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Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-MOV-2002) National Institutes of Health, Mammalian Submitted (01-MOV-2002) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PC C12P21/02,C12Q1/68//C12P21/08,G06F17/30,C12N15/00,C12N5/00 CC Primer for synthesizing full-length cDNA and use thereof FH Key Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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22-JAN-2002
07-JUL-2000 JP 2000253172
TOSHIO OTA, TETSUO NISHIKAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO
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  Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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100.0%; Prr
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Pred. No. 0.031;
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Park, J., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Rolfs, A., Hu, Y., Shen, B., Vannberg, F., Moreira, D., Relley, T., Zuo, D., Raphael, J., Baqui, M., Jepson, D., Harlow, B., LaBaer, J. and Brizuela, L.

Direct Submission

Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles St., Cambridge, MA, 02141-2023, USA

This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics, expression clones generated by Harvard colon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion (TM) cloning system between the SalI and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after last codon and before HindIII site to maintain reading frame.'
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1 (bases 1 to 1365)

1 (bases 1 to 1365)

1 (bases 1, Nu,Y., Shen,B., Vannberg,F., Moreira,D., Park,J., Rolfs,A., Hu,Y., Shen,B., Vannberg,F., Moreira,D., Kelley,T., Zuo,D., Raphael,J., Baqui,M., Jepson,D., Harlow,E., LaBaer,J. and Brizuela,L.

Cloning of human full-length CDS FLEXGene kinases in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1365 bp mRNA linear SYN 15-OCT-2003 Synthetic construct Homo sapiens death-associated protein kinase 3 AV315730
                                                                                                                                                                                                                                                                                                                                                                                                                       reading trame.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AY335738.1 GI:33304114 FLI_CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             recombinational vector system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTCATCACCTACATCCTGTGAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGTCATCACCTACATCCTGTGAGT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                                                                                                                                               clone="FLH000096.01L"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Vector: pBluescript"
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                                                                                                                                                                                                                                                                                                                                                                           . 1365
                                                                                                                                                                                                                                                                                                                          _type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.4%; Score 26;
100.0%; Pred. No.
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                                                                Stop->Leu"
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Best Local Similarity Matches 26; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg, L. J. Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
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Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,
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Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA secuences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus death-associated kinase IMAGE:4016911), complete cds.
NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Institute for Systems Biology
http://www.systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC022165.1
                                                                                                                                                                                                                                                Submitted (25-JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad.
22388257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                              Strausberg, R
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llarity 100.0%;
Conservative (
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AEEGLRELQRSRRLCHEDVEALAAIYEEKEAWYREESDSLGQDLRRLRQELLKTEALK
RQAQEEAKGALLGTSGLKRRFSRLENRYEALAKQVASEMRFVQDLVRALEQEKLQGVE
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. 0.029;
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se 2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1365;
                                                                  (LLNL)
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              JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                    VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 18
AB022341
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
                    Direct Submission
                                           2 (bases 1 to 2055)
Iwasaki,T., Murata-Hori,M. and Hosoya,H
                                                                                                                                                                                                     Murata-Hori,M., Suizu,F., Iwasaki,T., Kikuchi,A. and Hosoya,H. ZIP kinase identified as a novel myosin regulatory light chain
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                              ZIP kinase.
                                                                                                                            99283879
                                                                                                                                                   FEBS Lett.
                                                                                                                                                                                   kinase
                                                                                                                                                                                                                                                                                                                                                                                                                              AB022341.1
                                                                                               10356987
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RESULT 17 BC022165

DEFINITION

멍 S

ა 52

ORIGIN

Query Match

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

REFERENCE

AUTHORS

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL MEDLINE

PUBMED

TITLE

REMARK

cells

81-84

Chordata; Primates;

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

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445 CACCCCAACATCATCACGCTGCACGA 470
                                                                                                                                                                                     337 CACCCCAACATCATCACGCTGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 18 Row: f Column: 7.

Location/Qualifiers
              2055 bp
Homo sapiens mRNA for ZIP kinase,
AB022341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contact: amadan@systemsbiology.org
                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adan, Jessica Fahey, Erin Helton, Mark Ketteman,
Stephanie Rodrigues, Amy Sanchez and Michelle W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="S TKc; Region: Serine/Threonine catalytic domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="Dapk2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mol_type="mRNA"
strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                       'db_xref="CDD:smart00220"
GI:5162883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xref="MGI:1341297"
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100.0%; Pr
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Pred. No. 0.028;
0; Mismatches
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                                                                                                                                                                                     362
                                              complete
                                                                        mRNA
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                                                                                                                                                                                                                                                                                                                      Length 1883;
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DEFINITION
ACCESSION
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BD127287
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
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Best Local
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PATENTE: JP 2002017375-A 2718 22-JAN-2002;

HEIIX RESEARCH INSTITUTE
OS Homo sapiens (human)
PN JP 2002017375-A/2718
PD 22-JAN-2002
PF 07-JUL-2000 JP 2000253172
PF 07-JUL-2000 JP 2000253172
PI TOSHIO OTA, TETSUO NISHIXAWA, TAKAO ISOGAI, KOJI HAYASHI, SHIZUKO PI ISHII,
PI YURI KAWAI, AI WAKAMATSU, TOMOYASU SUGIYAMA, KEIICHI NAGAI, PI SHINICHI KOJIMA,
PI TETSUJI OTSUKI, HISASHI KOGA
PC C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC 10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            579 CAGTITCCTCAAGCAGATCCTGGACGG 604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2079)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BD127287
Primer for synthesizing
BD127287
                                                                                                                                                                                                                                                                                   Koga,
                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
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JP 2002017375-A/2718.
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                                                                                                                                                                                                                                          Primer for synthesizing full-length cDNA and use thereof Patent: JP 2002017375-A 2718 22-JAN-2002;
                                                                                                                                                                                                                                                                                               Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S., Kawai,Y., Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,T. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (12-JAN-1999) Hiroshi Hosoya, Faculty of Science, Hiroshima University, Department of Biological Science, Kagamiyama 1-3-1, Higashi-Hiroshima, Hiroshima 739-8526, Japan (E-mail:hhosoya@sci.hiroshima-u.ac.jp, Tel:81-824-24-7443,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fax:81-824-24-0734)
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/cell_line="HeLa RCB0007"
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mol_type="mRNA"
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Primer for synthesizing full-length cDNA and use thereof FH K
Location/Qualifiers
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                                                                                                                                                                                      /note=\overline{\ }cloning vector: pME18SFL3-mRNA from NT2 neuronal precursor cells after 2-weeks retinoic acid (RA)
                                                                                                                                                                                                                                                 /clOne="NT2RP2001529"
/cell line="NT2"
/cell type="teratocarcinoma"
/clone_lib="NT2RP2"
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/db_xref="taxon:9606"
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FUJISAWA PHARMACEUTICAL CO LTD, HIROYUKI MAMO
OS HOMO Sapiens (human)
PN WO 02070747-A/9
PN WO 02070747-A/9
PN WO 02070747-A/9
PD 12-SEP-2002 WO 2002JP001901
PR 01-MAR-2001 JP 01P 056438
PI 10-MAR-2001 JP 01P 056438
PI HIROYUKI MAMO
PC C1201/68,C1201/02,G01N33/15,C12N15/09,A61P35/02 CC
molecular diagnosis of chronic myelogenous leukemia FH
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AB007144
AB007144.1 GI:2911155
            Submitted (10-SEP-1997) Shizuo Akira, Hyogo College of Medicine, Department of Biochemistry, Mukogawa-cho 1-1, Nishinomiya, Hyogo 663, Japan (E-mail-akirabhyo-med.ac.jp, Tel:+81-798-45-6357, Fax:+81-798-46-3164)
                                                                    2 (bases 1 to 2105)
Akira, S. and Kawai, T.
Direct Submission
                                                                                                                                                                    Kawai,T., Matsumoto,M., Takeda,K., Sanjo,H.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                                                                                                                                        and Akira, S. which mediates
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AK097643
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Submitted (04-JUL-2002) Takao Isogai, FLJ Project(HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (B-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) MEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kanehori, K., Ishibashi, T., Chiba, Y., Fujimori, K., Hiraoka, S., Tanai, H., Watanabe, S., Ishida, S., Ono, Y., Hotuta, T., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Yamara, K., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Kimura, M., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oligo capping; fis (full insert sequence) Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 1 to 211 Isogai, T. and Yama Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK097643.1 GI:21757480
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AK097643
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sapiens cDNA FLJ40324 fis, clon
con sapiens mRNA for ZIP-Kinase.
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AEEGLRELQRSRRLCHEDVEALAAIYEEKEAWYREESDSLGQDLRRLRQELLKTEALK
RQAQEEAKGALLGTSGLKRRFSRLENRYEALAKQVASEMRFVQDLVRALEQEKLQGVE
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/mol_type="mRNA"
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and Yamamoto, J.
                                                                                                      Location/Qualifiers
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Pred. No.
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AR124102
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                                                                                                                                                                                                                                                                                 Unclassified.

1 (bases 1 to 2132)

Akira, S. and Kawai, T.

DNA coding for serine/threonine kinase

Patent: US 6171841-A 3 09-JAN-2001;

Location/Qualifiers
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AR124102
AR124102.
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DNA coding for serine/threonine kinase
Patent: US 5958748-A 3 28-SEP-1999;
                                                                                                                                                          Similarity
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larity 100.0%; I
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/clone_lib="TESTI2"
/note="cloning vector: pME18SFL3"
                                                                                                                                                                                                                                   /organism="unknown"
/mol_type="unassigned
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/mol_type="unassigned
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PN JP 199098984-A/1
PN JP 199098984-A/1
PD 13-APR-1997 JP 199
PF 26-SEP-1997 JP 199
PR SHIZUO SHINRA, TARR
PC C12N15/09, C12N1/2:
PC C12R1:19),
PC C12R1:19;
P
                                                                                                                                                                                                                                   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki,T. Primers for synthesising full-length cDNA and their use Patent: EP 1074617-A 14925 07-FEB-2001; Research Association for Biotechnology (JP)
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX880020 2224 bp DNA
Sequence 14925 from Patent EP1074617.
AX880020
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Patent: UP 1999098984-A 1 13-APR-1999;
SCIENCE & TECH AGENCY
OS Unidentified
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Shizuo, S. and Taro, K.
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C12N15/09, C12N1/21, C12N9/12//(C12N15/09,C12R1:91), (C12N1/21,
C12R1:19),
(C12N9/12,C12R1:19), C12N15/00, (C12N15/00,C12R1:91) CC
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13-APR-1999
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/codon_start=1
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/tanslation="MSTFROEDVEDHYEMGEBLGSGQFAIVRKCRQKGTGKEYAAKFI/translation="MSTFROEDVEDHYEMGEBLGSGQFAIVRKCRQKGTGKEYAAKFIKRRLSSSRRGVSREEIEREVNILREIRHPNIITLHDIFENKTDVVLILELVSGGELFCKRRLSSSRRGVSREEIEREVNILREIRHPNIITLHDIFENKTDVVLILELVSGGELFCKRLSSSRRGVSREEIEREVNILREIRHPNIITLHDIFENKTDVVLILELVSGGELFCKRRLSSSRRGVSREEIEREVNILDGVHYLHSKRIAHFDLKPENIMLLDKNVPNPRIKLI
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/mol_type="unassigned DN
/db_xref="taxon:9606"
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Pred. No. 0.028;
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CE 1 (bases 1 to 2224)

Ota,T. Isogai,T. Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J., Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T., Funahashi,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T., Funahashi,S., Seno,C. and Nezu,J.

Novel genes encoding protein kinase or protein phosphatase

AL Patent: WO 0109345-A, 6 08-FEB-2001;
Patent: WO 0109345-A, 6 08-FEB-2001;
Patent: WO 0109345-A, 6 08-FEB-2001;
PINAHASHI, KADRU SAITO, JUNICHI NAGAI,TETSUJI OTSUKI,SHINICHI FUNAHANI, RANGU SAITO, JUNICHI NAGAI,TETSUJI OTSUKI,SHINICHI FUNAHASHI, HIAKI SENO, JUNICHI NAGAI,TETSUJI OTSUKI,SHINICHI FUNAHASHI, PI 2000 WO 2000JP00560

PR 29-JUL-1099 JP 99P 248036,11-JAN-2000 JP 00P 118776 PR 29-JUL-1099 JP 99P 29-JUL-1099 JP 99P 29-JUL-1099 JP 99P 2
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Novel genes encoding protein kinase or protein phosphatase.
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WO 0109345-A/6.
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AEEGLRELQRSRRLCHEDVEALAAIYEEKEAWYREESDSLGQDLRRLRQELLKTEALK
RQAQEEAKGALLGTSGLKRRFSRLENRYEALAKQVASEMRFVQDLVRALEQEKLQGVE
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/mol_type="genomic DNA"
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Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Y. Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Y. Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K. and Otsuki Primer for synthesizing full-length cDNA and use thereof patent: JP 2002191363-A 12993 09-JUL-2002;
HELIX RESEARCH INSTITUTE
2 (bases 1 to 2224)
1 isogai, T. and Otsuki, T.
1 isogai, T. and Otsuki, T.
1 isogai, T. and Otsuki, T.
2 isogai, T. and Otsuki, T.
3 isogai, Helix Research Institute, Submitted (10-MAY-2001) Takao Isogai, Helix Research Institute, Submitted (10-MAY-2001) Takao Isogai, Chiba 292-0812, Japan Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
                                                                                                                                                 Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y., Nishikawa,T., Nagai,K., Sugano,S., Takahashi,Fujii,A., Hara,H., Tanase,T., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Nabekura,T., Ishii,S., Kawai,Y., Saito,K., Yamamotto,J., Wakamatsu,A., Nakamura,Y., Nagahari,K., Masuho,Y. and Oshima,A. WEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AK027590 2224 bp mRNA linear Homo sapiens cDNA FLU14684 fis, clone NT2RP2004933, to Homo sapiens mRNA for ZIP-kinase.
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BD158150.1 GI:2786390
JP 2002191363-A/12993.
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      oligo capping; fis (full insert sequence).
Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                     AK027590
AK027590.1 GI:14042369
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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KEIICHI NAGAI,TETSUJI OTSUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000 JP 2000280990
TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI,KAORU
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JP 2002191363-A/12993
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Location/Qualifiers
(215). (1576).
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100.0%; Pred. No. 0.4
/ative 0; Mismatches
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highly similar
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AC011488/c
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Best Local S
Matches 26
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                   Query Match
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Best Local Similarity
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Submitted (01-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Submitted (01-AUG-2002) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Aug 1, 2002 this sequence version replaced gi:9256301.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                             Finishing Completed at Stanford Human www-sigc.stanford.edu
Quality: Phrap Quality >=40 100% of Se
Estimated Total Number of Errors is 0.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, US3 (bases 1 to 134308)
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DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing and clone selection: Helix Research Institute (supported by Japan Key Technology Center etc.) and Department of Virology, Institute of Medical Science, Industries, of Tology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 134308)
DOE Joint Genome Institute.
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AC011488
AC011488.7 GI:22038500
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                                                                            /chromosome="19"
/clone="CTB-171N13"
                                                                                                                  organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="NT2RP2004933"
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/cell_type="teratocarcinoma"
/clone_lib="NT2RP2"
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. 0.028;
DB 9;
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CTB-171N13, complete sequence.
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AC124439
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AC124439
AC124439.4
                                                                                             Submitted (13-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Mar 1, 2003 this sequence version replaced gi:27764792.
                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Direct Submission
Submitted (14-JUN-2002) Genome Sequencing
or Touris, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 162530)
Berghoff,A., Cotton,M., Meyer,R. and Bielicki,L.
The sequence of Mus musculus BAC clone RP24-261N14
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26;
                                                                                                                                                                                                         Submitted (01-MAR-2003) Genome Parkway, St. Louis, MO 63108,
                                                                                                                                                                                                                                                        5 (bases 1 to 162530)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                       Submitted (16-JAN-2003)
Parkway, St. Louis, MO
                                                                                                                                                                                                                                                                                                                                      4 (bases 1 to 162530)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 162530)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing of Mus musculus 
Unpublished (2001)
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Mus musculus BAC clone RP24-261N14
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                                                                                                                                                                                          kway, St. Louis, MO (bases 1 to 162530)
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Center project name: M_BB0261N14
                            Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                Center: Washington University Genome Center code: WUGSC
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence restriction This sequence was finished as follows unless otherwise noted: from more than one subclone; digest. γď

MAPPING INFORMATION:
Mapping information for
Department of Genetics, this clone was provided by Washington University, St. Dr. Wes Warren, Louis MO. For

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The RPCI-24 BAC Library has been constructed by Pieter de Jong and coworkers (http://www.chori.org) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       additional information about the map position of this sequence, see http://genome.wustl.edu % \left( 1\right) =\left( 1\right) +\left( 1\right) =\left( 1\right) +\left( 1\right) +\left( 1\right) =\left( 1\right) +\left( 1\right)
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This sequence is the entire insert of the clone.
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9193. .9303
                                                                                                                                                                                                                                                       /rpt_family="Alu"
9567. .9782
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/mol_type="genomic_DNA"
/db_xref="taxon:10090"
/chromosome="9"
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10168. .10291
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                                                              rpt_family="Alu" 0293. .10485
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one_lib="RPCI-24"
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_ .4972
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_ .3436
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26; Conserv
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Larity 100.0%; Pred. No. 0.02;
Conservative 0; Mismatches 0
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18468. .18581
/rpt_family="Alu"
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10832. .10970
/rpt_family="B4"
10986. .11005
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rpt_family="ID"
3254. .13392
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213. | 16677
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233. .18260
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27. .11252
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5 family="Alu"
73. .14983
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[. .18419
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FEATURES	TITLE JOURNAL COMMENT	TITLE JOURNAL REFERENCE AUTHORS	RESULT 33 ACOL5914 LOCUS
http://ftp.genome.washington.edu/RM/RepeatMasker.html	McEwan, P., McEvanan, K., Meldrin, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission L Submitted (28-UUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 28, 2002 this sequence version replaced gi:18482289. All repeats were identified using RepeatMasker:	Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehocky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M. Direct Submission Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 170078) Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Birren, B., Linton, L., Wusbaum, C., Lander, E., Ali, A., Allen, N., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, M., MacLean, C., Laroccan, C., Macdonald, M., MacLean, C., Laroccan, C., Macdonald, M., MacLean, C., Laroccan, K., Lamazares, R., MacLean, C., Laroccan, M., MacLean, C., Laroccan, C., Macdonald, M., MacLean, C., Laroccan, C., Laroccan, C., MacLean, C., Laroccan, C., Laroccan, C., MacLean, C., Laroccan, C., Laroccan, C., Laroccan, C., MacLean, C., Laroccan, C., Laroccan, C., Laroccan, C., MacLean, C., Laroccan, C., Lar	ACC15914 170078 bp DNA linear PRI 28-JUN-2002 HOmo sapiens chromosome 15, clone RP11-111214, complete sequence. ACC15914.8 GI:21622757 HTG. HOmo sapiens (human) Homo sapiens (human) Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 170078) Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 15, clone RP11-111E14 Unpublished 2 (bases 1 to 170078) Baldwin,J., Barna,N., Beckerly,R., Boguslavkiy,L., Boukhgalter,B., Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A., Cocke, P., Dearellano, K., Dewar,K., Domano,M., Domelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
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O'Donnell, P., Olivar, T.M., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W. 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Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic, Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travi., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
------ Project Information
Center project name: L5589
Center clone name: 505_L_16
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8698. .9010
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                        /rpt_family="MIR" 13677. 1205.
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complement(11093..11402)
/rpt_family="Alusx"
complement (15473. .15602)
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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             family="MIR"
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26; Conserv
                                                                 AC034201.2 GI:12965321
HTG; HTGS_PHASE1; HTGS_DRAFT.
Homo sapiens (human)
                                                                                                                 210617 bp DNA linear HTG 20.
Homo sapiens chromosome 19 clone CTB-172H21, WORKING DRAFT
SEQUENCE, 35 unordered pieces.
AC034201
DOE Joint Genome Institute.
         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 210617)
                                                     Homo sapiens
                                                                                                                                                                                                                                                                                   2.4%; Score 26; DB 9; ilarity 100.0%; Pred. No. 0.02; Conservative 0; Mismatches
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complement(20150. .20326)
/rpt family="MIR"
20403. .2047
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17007. .17057
/rpt_family="MER115"
17296. .17339
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                                                                                                                                                                                                                                                                                                                                        complement(26176...26476)
/rpt_family="AluSx"
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complement(24399. .24
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complement(19361
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18583. .18077
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0538. 20821
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Consensus quality: 178878 bases at least Q40
Consensus quality: 191077 bases at least Q20
Consensus quality: 196408 bases at least Q20
Estimated insert size: 138740; agarose-fp estimation
Estimated insert size: 138740; agarose-fp estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 8.87 in Q20 bases; sum-of-contigs estimation
**NOTE: This is a 'working draft' sequence. It currently
**consists of 35 contigs. The true order of the pieces
**is not known and their order in this sequence record is
** arbitrary. Gaps between the contigs are represented as
** runs of N, but the exact sizes of the gaps are unknown.
** This record will be updated with the finished sequence
** as soon as it is available and the accession number will
** be preserved.
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Center Project Name: 130441, BC95464
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Center Code: JGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 210617)
DOE Joint Genome Institute.
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Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Web site: http://www.jgi.doe.gov
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2 (bases 1 to 224148)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Forrest, C., Fucke, R., Gage, D., Ferreira, P., Fitzhugh, W., Forrest, C., Fucke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
                                                                                                                                                                                                               1 (bases 1 to 224148)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 15, clone RP11-652K13
Unpublished
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE, 40 unordered pieces.
ACO16179
ACO16179.6 GI:14336574
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
HTGMO SEQUENS (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC016179 224148 bp DNA linear 1 Homo sapiens chromosome 15 clone RP11-652K13 map 15,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
/chromosome="19"
/clone="CTB-172H21"
/clone="CTB-172H21"
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87764: contig of 5199 bp in le
87864: gap of unknown length
95881: contig of 8117 bp in le
95081: gap of unknown length
108564: gap of unknown length
108664: gap of unknown length
124079: gap of unknown length
14002: contig of 15315 bp in l
140702: gap of unknown length
140602: contig of 16523 bp in l
140702: gap of unknown length
174140: contig of 36377 bp in l
174240: gap of unknown length
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g of 7722 bp in 16
g of 7722 bp in 16
g of 9262 bp in 16
g of 9262 bp in 16
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g of 5199 bp in 16
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HTG 11-JUN-2001 , WORKING DRAFT

Doyle, M.,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (23-NOV 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jun 11, 2001 this sequence version replaced gi:13621297.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center project name: L4221
Center clone name: 652 K 13
Consensus quality: 204388 bases at least Q40
Consensus quality: 204388 bases at least Q30
Consensus quality: 212270 bases at least Q30
Consensus quality: 212370 bases at least Q30
Consensus quality: 212370 bases at least Q30
Consensus quality: 212370 bases at least Q30
Insert size: 194000; agarose-fp
Insert size: 220488; sum-of-configs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality coverage: 6.5 in Q20 bases; agarose-fp Quality coverage: 5.7 in Q20 ba.

NOTE: This is a 'working draft' sequence. It currently consists of 40 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it
be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
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Center: Whitehead Institute/ MIT Center for Genome
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contig of 710 bp
gap of 100 bp
contig of 688 bp
gap of 100 bp
contig of 602 bp
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5017. .5511
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4 223343: gap of 100 bp
4 224148: contig of 805
coation/Qualifiers
                                                                                note="assembly_fragment"
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                                                                                                                                                                                                                                                                                                  clone="RP11-652K13"
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?23243: contig of 34648 bp in length
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contig of 13307 bp i
gap of 100 bp
contig of 25743 bp i
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of 100 bp
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of 100 bp
ig of 15329 bp in length
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f of 1396 bp
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of 1113 bp
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2749 bp in length
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841 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
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DEFINITION
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AC096406
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ORGANISM
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Nuzny, D. Marie, Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranake, D., Barber, M., Barnstead, M., Benahmed, F.,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., P'Souza, L.,
Davila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dumn, A., Durbin, K., Duvall, B., Baves, K.,
Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
Harvey, Y., Havlak, P., Haddun, S.L., Hamilton, C., Hamilton, K.,
Hernandez, R., Hines, S., Hladdun, S.L., Hodgson, A., Hendandz, J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            923 GGCGTCATCACCTACATCCTGTGAGT 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC096406 228405 bp Dr
Rattus norvegicus clone CH230-62C22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC096406.6 GI:30520479
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/note="assembly_fragment"
8060. .8731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
19567. .20377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_fragment'
17949. .19466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment"
14410. .15805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="assembly_fragment"
9709. .10418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
16816. .17848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_fragment"
15906. .16715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
13469. .14309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_fragment"
12897. .13368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="assembly_fragment'
6551..7042
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12009. .12796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
10519. .11206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="assembly_fragment"
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Pred. No. 0.019;
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2, WORKING DRAFT SEQUENCE:
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REFERENCE AUTHORS TITLE JOURNAL

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Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jackson, L., Jalang, H., Johnson, B., Johnson, R., Jolivet, A., Karpethy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Kovar, C., Maheshwari, M., Mahidarthe, M., Mahmoud, M., Malloy, K., Mangum, A., Mahoud, M., Malloy, K., Mangum, A., Mahoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., McNeill, T.Z., Menen, E., Milosa, M., Wartin, R., Martinez, E., Milosa, M., Murphy, M., Nair, L., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Mangeon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Roidkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, M., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Shetty, G., Scherer, S., Sott, G., Shatsman, S., Shen, H., Shetty, J., Shotty, A., Tabor, P., Taylor, C., Taylor, C., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Wango, O., Wang, S., Wuldron, L., Waldron, L., Walker, B., Wang, J., Zhou, J., Zhou, J., Zhou, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, J., Zhou, S., Dunn, D., Yoon, V., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
                                                                                                                                                                                                                                              Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:24819671.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shorgun sequence reads. Both end sequences and whole genome sequence contents with the individual sequences and whole genome sequence reads.
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Direct Submission
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat Genome Sequencing Direct Submission
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                                                                                                                                                                                                             shotgun sequence only contigs will be indicated
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Center: Baylor College of Medicine Center code: BCM
                                                                                                               Genome Center
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Best Local .
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Nuzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
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Clacko, J., Chavez, D., Chen, G., Coyle, M., Cree, A., D'Souza, L.,
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Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
Bgan, A., Escotto, M., Bugens, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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Rattus norvegicus clone CH230-98D19,
                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 228405: contig of 228405 bp in length.

Location/Qualifiers
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NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes.
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225678. .228405
/note="wgs_end_extension
clone_end:T7"
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clone_end:T7
site:EcoRI
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complement(223054...22)
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clone_end:Sp6
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|mol_type="genomic DNA"
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Center project Information
Center project name: GHTS
Center clone name: CH230-98D19
-----Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 215152 bases at least Q40

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Center: Baylor Co

College

of Medicine

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Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gubregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Kelly, S., King, L., Koyar, C., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Louiseged, H., Lozado, R.J., Lu, X., Ma, J., Lowis, C., Kraft, C.L., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahindartne, M., Martin, R., Martinez, E., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mahmoud, M., Mahinday, S., McLeod, M. P., McNeill, T.Z., Meenen, E., Morgan, M., Morris, S., Munidasa, M., Murphy, M., Naikervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Manoud, M., Martin, R., Parks, K., Parks, K., Parks, K., Martin, R., Perez, A., Perez, L., Pipper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L. Plapper, F., Poindexter, A., Popovic, D., Primus, E., Pul, L.-L. Plapper, F., Roilly, M., Ren, Y., Revees, K., Reigh, R., Shety, J., Sherer, S., Scott, G., Shatsman, S., Shen, H., Shety, J., Sherer, S., Scott, G., Shatsman, S., Shen, H., Shety, J., Sherer, S., Scott, G., Shatsman, S., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Williams, G., Warren, N., Warren, R., Weiz, R., Wang, J., Warren, R., Weiz, R., Woclen, H., Wong, J., Warren, R., Weiz, R., Wolter, B., Wang, J., Warten, S., Shath, D., Waldon, H., White, F., Wang, J., Yakub, S., Yen, J., Yoon, L., Woon, V., White, F., Wang, J., Wallson, R., Smith, D.R., Holt, R., Smith, H.O., Weinstock, G., and Gibbs, R.A.
                                                                          Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Baylor Plaza, Houston, TX 77030, USA
On May 10, 2003 this sequence version replaced gi:25008467.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-NOV-2001) Human Genome Sequencing of Molecular and Human Genetics, Baylor College Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 (bases 1 to 232704)
Worley, K.C.
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Rat Genome Sequencing Consortium
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Genome Center
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                                     Submitted (21-DEC-2002) Genome Sequencing Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 184961) McPherson, J.D. and Waterston, R.H. Direct Submission
                                                                                                                                                                                      Direct Submission
Direct Submission
Submitted (24-JUL-2002) Genome Sequencing
Submitted (24-JUL-3002) Genome Sequencing
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Mus musculus BAC clone RP23-312H15 from 16,
AC129021
AC129021.4 GI:27657604
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26; Conserv
                                                                                                                                                       Parkway, St. Louis, MO 63108, USA 4 (bases 1 to 184961)
McPherson, J.D. and Waterston, R.H.
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McPherson, J.D. and Waterston, R.H.
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Belter, E., Haakenson, W. and Kozlowicz, A.
The sequence of Mus musculus BAC clone RP23-312H15
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                       Wilson, R.
Parkway,
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                        bases 1 to 184961)
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(12-JAN-2003) Genome Sequencing St. Louis, MO 63108, USA
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_xref="taxon:10116"
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100.0%; Pred. No. 0.0
1ve 0; Mismatches
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                                                                                                                                           Submitted (08-NOV-2003) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, On Jan 12, 2003 this sequence version replaced gi:27356760.
                                                                                                                                                                                                                                                           Parkway, St. Louis, MO (bases 1 to 184961)
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Submitted (25-MAR-2003)
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McPherson, J.D. and Wat
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Center project name: M_BA0312H15
                      Contact: submissions@watson.wustl.edu
                                                                                  Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                Web site: http://genome.wustl.edu
                                                                                                                            ---- Genome Center
                                                                                                                                                                                                                                                                                                                                      and Waterston, R.H.
                                                                                                                                                                                                                                                                          63108,
                                                                                                                                                                                                                                                                            ne Sequencing Center, 4444 Forest Park
USA
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clone sections once, or longer becaus between neighboring data submissions. NOTICE: This sequence may not represent the entire insert of this It may be shorter because we only sequence overlapping or longer because we provide a small overlap

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >: 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, se http://genome.wustl.edu MAPPING INFORMATION: See

# SOURCE INFORMATION:

The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/6J mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of overlapped by ACO87900. the clone. This clone is

FEATURES source repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region repeat\_region /rpt\_family="B4" 4004. .4117 /rpt\_family="B2" 2029. .2131 /rpt\_family="Alu" 4150. .4451 /rpt\_family="Alu" 2236. .2377 Location/Qualifiers rpt\_family="Alu" 'clone="RP23-312H15" map="16 'chromosome="16" 'db\_xref="taxon:10090' organism="Mus musculus" rpt\_family="MaLR" \_family="MaLR" type="genomic DNA"

repeat\_region repeat\_region

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/rpt_family="Malk"
22711. .2285p
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/rpt_family="Alu"
4866. .4960
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8322. .8687
                                                                                                      /rpt_family="RMER1A" 22169. .22263
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13497. .13607
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7751. .7898
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7429. .7554
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18451. .18597
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17917. .18130
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17382. .17545
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16867. .17334
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10379. .10480
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10163. .10220
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5006. .5152
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16354. .16723
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| family="Alu"
| 20. .21654
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_family="ID"
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3. .10640
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_family="Alu"
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Matches 25; Conserv
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            5 (bases 1 to 195066)
Cox, T., Shaull, S., Yao, Z. and Roe, B.A.
Direct Submission
Submitted (14-NCV-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
6 (bases 1 to 195066)
                                                                                                                                                                                                                                                                                                                                  Cox,T., Shaull,S., Yao,Z. and Roe,B.A.
Direct Submission
Submitted (66-FEB-2001) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
3 (bases 1 to 195066)
Cox,T., Shaull,S., Yao,Z. and Roe,B.A.
Direct Submission
Submitted (01-NOV-2001) Department Of Chemistry And Biochemistry,
Direct Submission
Submitted (01-NOV-2001) Department Of Chemistry And Biochemistry,
OK 73010 (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (1980) (
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4 (bases 1 to 195066)
Cox.T., Shaull, S., Yao, Z. and Roe, B.A.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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1 (Cox.T., Shaull,S., Yao,Z. and Ree,B.A.
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Mus musculus clone rp23-17116 map
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24854. .24995
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. 0.07;
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19 strain C57BL/6J, complete
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Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                Cloning of the mitogen-activated S6 kinase from rat liver reveals an enzyme of the second messenger subfamily Proc. Natl. Acad. Sci. U.S.A. 87 (19), 7365-7369 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rat S6 kinase mRNA,
M57428 M35864
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On Nov 14, 2002 this sequence version replaced gi:22038563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cox,T., Shaull,S., Yao,Z. and Roe,B.A.
Direct Submission
Submitted (18-SEP-2003) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                        Original source text: Rat
                                                                                                                                                                                                                                                                    Lane,H.A., Morley,S.J., Doree,M., Kozma,S.C. and Thomas,G. Identification and early activation of a Xenopus laevis p70s6k following progesterone induced meiotic maturation EMBO J. 11 (5), 1743-1749 (1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                 Thomas,G
                                                                                                                                                                                                                                                                                                                                                                                                                                              Kozma, S.C., Ferrari, S., Bassand, P., Siegmann, M.,
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/clone_lib="RPCI - 23 Female (C57BL/6J) Mouse BAC
/gene="S6 kinase"
                /gene="S6 kinase"
134. .1642
                                                                                         /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/tissue_type="liver"
                                                                                                                                       organism="Rattus norvegicus"
(mol_type="mRNA"
                                                                                                                                                                                        Location/Qualifiers
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/mol_type="genomic DNA"
/strain="C57BL/6J"
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                                                                        dev_stage="7-8 week"
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                                             .ssue_lib="stratagene lambda zap II 936507"
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716 GACCTGAAGCCGGAGAACATCATG 739
                                              642 GACCTGAAGCCGGAGAACATCATG 665
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                                                                                                  Conservative
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                                                                                                                        2.2%;
                                                                                                  .
.
                                                                                                                      Score 24;
Pred. No.
                                                                                                  Mismatches
                                                                                                                        DB 10;
                                                                                                  0
                                                                                                                                                 Length 1800;
                                                                                                  0
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Strauberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsleh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,

Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyaki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Ketteman, M., Madan, A., Rodrigues, S.,

Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) Submitted (04-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, BC038491 1846 bp Mus musculus RIKEN cDNA 2610318I15 NIH-MGC Project URL: http://mgc.nci.nih.gov Direct Submission Strausberg, R. human and mouse cDNA sequences Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002) Eukaryota; Mammalia; I Mus musculus Mus musculus (house mouse) MAGE:4010710), (bases 1 to 1846) (bases 1 to 1846) Eutheria; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus GI:23512345 complete cds mRNA gene, linear ROD 07-OCT-2003 mRNA (cDNA clone MGC:47115

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ORIGIN
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                         LOCUS
DEFINITION
                                                                                                   RESULT 43
     ACCESSION
                                                                          RATS6PK
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
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                                                                                                                                                                                                                         642
                                                                                                                                                                           726 GACCTGAAGCCGGAGAACATCATG 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc.mgc@nhgri.nih.gov
Akhrer, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Gupta, J., Haghighi, P.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Laric, P., Legaspi, R.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.
RATS6PK 2287 bp mF Rat S6 protein kinase mRNA, complete M58340 M37777
                                                                                                                                                                                                                                                                    l Similarity
24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINI at: http://image.llnl.gov Series: IRAK Plate: 80 Row: f Column: 8
This clone was selected for full length sequencing because it passed the following selection criteria: GenomeScan gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prediction
                                                                                                                                                                                                                         GACCTGAAGCCGGAGAACATCATG 665
                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /protein_id="AAH38491.1"
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catalytic domain"
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KEPENIMLMIQGHVKLIDFGLCKESIHDGTVYHTFGCTIEYNAPEILKRSGHNRAVDW
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FSPGDFWGRGASASTANPQTPVEYFMETSGIEQMDVTVSGEASAPLPIRQPNSGPYXK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAFPMISKRPEHLRMNL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="CDD:smart00220"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          db_xref="LocusID:72508"/db_xref="MGI:1919758"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  clone_lib="NCI_CGAP_Lu30"
|lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   strain="CZECH II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ocation/Qualifiers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="2610318I15Rik"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                        100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 type="Mammary tumor metastatized to lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         National Institutes of Health Intramural (NISC),
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                           Score 24; DB 10;
Pred. No. 0.36;
                                                                                                                                                                                                                                                                       Mismatches
                                                   mRNA
                              cds.
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                  Length 1846;
                                                                                                                                                                                                                                                                       Indels
                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          protein kinases,
                                                     ROD 27-APR-1993
                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                       0;
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MEDLINE
PUBMED
COMMENT
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ORGANISM
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KEYWORDS
                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                   VERSION
KEYWORDS
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AL604063/c
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                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                           AUTHORS
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Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
Submitted (29-NOV 2001) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Nov 30, 2001 this sequence version replaced gi:16444787. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M58340.1 GI:206841
S6 protein kinase; insulin/mitogen stimulated protein kinase; p70
S6 protein kinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Ro
1 (bases 1 to 146759)
                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Original source text: Rat,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91046033
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Banerjee, P., Ahmad, M.F.,
                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                               Lovell, J
                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                 AL604063.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AL604063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complete sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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QAFPMISKRPEHLRMNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad. Sci. U.S.A. 87 (21), 8550-8554 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             db xref="taxon:10116"
/cell_line="harata"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .2287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _line="hepatoma line H4IIEC3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _lib="lambda gt11 PB4"
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om clone RP23-467J12 on chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 24;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cDNA to mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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REFERENCE
AUTHORS
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VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEYWORDS
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
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Nuzny, D. Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blach, D., Burber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blach, D., Burch, D., Burch, P., Burch, P., Brown, M., Center, A., Char, K., Cavazos, I., Ceasar, H., Center, A., Char, Y., Chen, Z., Chu, J., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Clacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Cree, A., D'Souza, L., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Durn, A., Burbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35687 GACCTGAAGCCGGAGAACATCATG 35664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     642 GACCTGAAGCCGGAGAACATCATG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SMISSPROT; Tr., TREMBL; Wp:, WORMPEP; Information on the WORMPEP databases can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED RAttus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AC128095
AC128095.3 GI:25080727
HTG; HTGS PHASE1; HTGS |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus clone CH230-319P22, ***
***, 3 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RP23-467J12 It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP23-366M19 is at 144760 in this sequence. The true right end of clone RP23-259D24 is at 2000 in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C elegans/wormpep RP23-467J12 is from the RPCI-23 Mouse PAC Library—constructed by the group of Pieter de Jong.
For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VECTOR: pBACe3.6
IMPORTANT: This sequence is not the entire insert of clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 243780)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2.2%; Score 24;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 146759;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.25;
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

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ORIGIN

RESULT

REFERENCE AUTHORS TITLE JOURNAL

COMMENT

Center project name: GZQP
Center clone name: CH230-319P22
Center Summary Statistics
Assembly program: Phrap; version 0.990329

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu

Consensus quality: 185810 bases at Consensus quality: 190701 bases at Consensus quality: 194362 bases at

least Q40 least Q30 least Q20

SOURCE

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AL Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 19, 2002 this sequence version replaced gi:23195451.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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Lorensuhewa, L. Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
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Williams, G., and Gibbs, R.A.
Diter, Submission
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Direct Submission
Submitted (19-UUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Davolor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished 2 (bases 1 to 243780)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
Center: Baylor Co
Center code: BCM
Web site: http://
                                                                                                                                                                                                                                     ----- Genome Center
                                                                                                                                      Collège of Medicine
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FEATURES
source
Search completed: June 30, 2004, 20:19:56
Job time : 4628 secs
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                                                                                                                                                                             Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                      174521 GACCTGAAGCCCGGAGAACATCATG 174544
                                                                                                                                  642 GACCTGAAGCCGGAGAACATCATG 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data.html).

* NOTE: This is a 'working draft' sequence. It currently

* consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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134223
223290
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223390
                                                                                                                                                                             2.2%; Score 24; DB 2; llarity 100.0%; Pred. No. 0.24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 134122: contig of 134122 bp in length 134222: gap of unknown length 223289: contig of 89067 bp in length 223389: gap of unknown length 243780: contig of 20391 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence:BZ147671"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         .51649
                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                             Length 243780;
                                                                                                                                                                                    0
                                                                                                                                                                                  Gaps
                                                                                                                                                                                    0;
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В Ś

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Command line parameters:

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-DEV_TIMEOUT=10 -VGAPPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                      No
                                                                                                                                                                                                                                                                                                                                                                          score g
  No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xgapop 10.0,
Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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1: /cgn2_6/ptodatta/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodatta/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
6: /cgn2_6/ptodata/2/ina/Dackfiles1.seq:*
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US-09-159-385-4
US-09-186-277-4
US-09-186-277-3
US-09-186-277-3
US-09-186-277-3
US-08-631-097-3
US-08-631-097-3
US-09-428-711A-15
US-09-800-960-1
US-09-800-960-1
US-09-733-388-3
US-09-733-388-1
US-09-733-388-5
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Sequence 3, Appli
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Sequence 9, Appli
Sequence 15, Appli
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quence 26, quence 21, quence 21, quence 21, quence 1, quence 3, quence 4, quence 61, quence 10, quence 10, quence 11, quence 11,	equence 526, Applequence 1, Applequence 3, Applequence 12, Applequence 12, Applequence 851, Applequence 26, Ap

## ALIGNMENTS

US-09-159-385-4

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Sequence 4, Application US/09159385
Patent No. 5958748
GENERAL INFORMATION:
APPLICANT: RAWAL, TARO
ITILE OF INVENTION DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: PH-569
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: JP97/261589
EEARLIER FILING DATE: 1997-09-26
INUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 1429
TYPE: DNA
CRGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (10)...(1353)
US-09-159-385-4

Alignment Scores:
Pred. No.:
Pred. No.:
Percent Similarity: 73.82%
Best Local Similarity: 69.96%
Cuery Match: 40
DB:
FIGURE9 (1-361) x US-09-159-385-4 (1-1429)
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99

PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe 116

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APPLICANT: AKIRA, SHIZUO
APPLICANT: KAWAI, TARO
TITLE OF INVENTION. DNA CODING FOR SERINE/THREONINE KIN
FILE REFERENCE: 081356/0128
CURRENT APPLICATION NUMBER: US/09/186,277
CURRENT FILING DATE: 1999-11-05
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
TENGRUE: 1420
Score:
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US-09-186-277-4
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                                                                LENGTH: 1429
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: CDS
LOCATION: (10)..(1353)
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GENERAL INFORMATION:
APPLICANT: RAKIRA, SHIZUO
APPLICANT: RAKIRA, SHIZUO
APPLICANT: RAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/TH
FILE REFERENCE: PH-569
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: UP97/261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PALENTIN VEY. 2.0
SEQ ID NO 3
LENGTH: 2132
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3, Application US/09159385
Patent No. 5958748
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Best Local Similarity:
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                       spMetProGlyProHisGln 357
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RESULT

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GENERAL INFORMATION:
APPLICANT: AKKRA, SHIZUO
APPLICANT: KAWAI, TARO
APPLICANT: KAWAI, TARO
ITILE OF INVENTION: DNA CODING FOR SERINE/THREONINE KIN
FILE REFERENCE: 081356/0128
CURRENT APPLICATION NUMBER: US/09/186,277
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
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NAME/KEY: CDS
LOCATION: (94)..(1455)
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ORGANISM: Homo
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Patent No. 596881
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TELEFAX: (202)473-6915
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                       MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: No
ANTI-SENSE: No
FRAGMENT TYPE: No. 5968816 applicable
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                  NAME: Cohen, Herbert
REGISTANT NUMBER: 25,109
REFERENCE/DOCKET NUMBER: 07-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)463-7700
               TISSUE TYPE: blood
CELL TYPE: Leucocyte
CELL LINE: HeLa
ORGANELLE: not applicable
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: POT/US94/11598
FILING DATE: 12-Oct-94
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
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                                                                         STRAIN: not applicable
INDIVIDUAL ISOLATE: not applicabl
DEVELOPMENTAL STAGE: not applicabl
HAPLOTYPE: not applicable
TISSUE TYPE: blood
                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/631,097 FILING DATE: 12-Apr-96 CLASSIFICATION: 514
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SOFTWARE: ASCII
   LIBRARY:
                                                                                                                                                              ORGANISM:
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Query Match:
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; PUBLICATION INFORMATION:
US-08-631-097-3
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Sequence 9, Application US/08810712G
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IDENTIFICATION METHOD: in specification
OTHER INFORMATION: prevention of IFN-2
OTHER INFORMATION: promoted cell death
UBLICATION INFORMATION: not available
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GENERAL INFORMATION:
APPLICANT: Yeda Research and Development Co. LTD
INTEL OF INVENTION: Tumor Suppressor Genes, Proteins
ITILE OF INVENTION: Use of said Genes and Proteins
FILE REFERENCE: sequencelist
CURRENT APPLICATION NUMBER: US/08/810,712G
CURRENT FILING DATE: 1997-03-03
EARLIER APPLICATION NUMBER: PCT/US94/11598
EARLIER FILING DATE: 1994-10-12
NUMBER OF SEQ ID NOS: 31
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
SOFTWARE: DNA
ROANISM: Homo sapiens
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Query Match:
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APPLICANT: Tohinasawa, Takuji
APPLICANT: Tohinasawa, Takuji
APPLICANT: Tohinasawa, Takuji
APPLICANT: Shirasawa, Takuji
APPLICANT: Shirasawa, Takuji
APPLICANT: No. 6358720uchi, Teruhisa
TITLE OF INVENTION: SBRINE/FREONINE PROTEIN KII
FILE REFERENCE: 06501-045001
FILE REFERENCE: 06501-045001
FILE APPLICATION NUMBER: US/09/428,711A
CURRENT FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: PCT/PP98/01246
PRIOR APPLICATION NUMBER: JP 9/124798
PRIOR APPLICATION NUMBER: JP 9/124798
PRIOR FILING DATE: 1997-04-28
NUMBER OF SEO 1D NOS: 21
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US-09-428-711A-15
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SEQ ID NO 15
LENGTH: 522
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
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NAME/KEY: CDS
LOCATION: (269)...(3418)
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                                                                                                                                                                                                                           ---TCTCAGACGCTGCTGGGGAAGGAAATCAAAATCCTGAAGGAAACATGAAAAC
                                                                                                                                                                                                                                                           ValSerArgGluGluIleGluArgGluValSerIleLeuArgGluIleArgHisProAsn 148
                                                                                                                                                                                                                                                                                                                        GATTTGGAGGTCGCCGTCAAGTGCATTAACAAGAAGAACCTCGCCAAG-------
                                                                                                                                                                                                                                                                                                                                                            GlyMetGluTyrAlaAlaLysPheIleLysLysArgArgLeuProSerSerArgArgGly 128
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                                                                                                                                   ATCGTGGCCCTGTACGACTTCCAGGAAATGGCTAATTCTGTCTACCTGGTTATGGAGTAC
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ProArgSerSerSer---SerArgSerTrpThrValSerThrThrCysThrProSerAla
                                           TGCAACGGTGGGGACCTGGCCGACTACCT-GCACGCCATGCGCACGCTGAGCGAGG-ACA
                                                                                                                                                                               IleIleThrLeuHisAspValPheGluAsnLysThrAspValValLeuIleLeuGluLeu 168
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202 430

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242

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310

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GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE F
TITLE OF INVENTION: ACID MOLECULES ENCODING
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOIIS
CURRENT APPLICATION UMBER: US/09/800,960
CURRENT FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                 ; SOFTWARE: FastSE(
SEQ ID NO 1
; LENGTH: 2061
; TYPE: DNA
; ORGANISM: Human
US-09-800-960-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT B
US-09-800-960-1
, Sequence 1, Application US/09800960
, Patent No. 6387677
                                                                                                                                                                                                                                       Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                 FIGURE9
                                                                                                                                                                                                                                                                                                                           Alignment Scores: Pred. No.:
                                                                                                                                                                                 (1-361) \times US-09-800-960-1
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                                                                                                                                      LeuGlySerSerValValValGlyAsnLeuGlyThrAspAlaGlnArg-------
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                 CTGCACCGCCGCCCGCCCGCCCGCCAGCATGGCCACCGCCACCGCCACCGCTTTC
                                                        LeuGlyTyrArgValLeu---ProSerSerGlySerAlaAlaLeuSerCysSer-----
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Matches:
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Mismatches:
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                                                                       PRIOR APPLICATION NUMBER: 09/800,960
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.
SEQ ID NO 1
LENGTH: 2061
TYPE: DNA
ORGANISM: Homo sapien
US-10-096-960-1
                 Alignment Scores
Pred. No.:
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                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: YE, Jane et al.
APPLICANT: YE, Jane et al.
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS,
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOO1158DIV
CURRENT APPLICATION NUMBER: US/10/096,960
CURRENT FILING DATE: 2002-03-14
CURRENT FILING DATE: 2002-03-14
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Applic
Patent No. 6664085
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Sequence 3, Application US/09733388
Patent No. 6602698
GENERAL INFORMATION:
APPLICANT: Donoho, Greg
APPLICANT: Scoville, John
APPLICANT: Turner, C. Alexander Jr.
APPLICANT: Friedrich, Glenn
APPLICANT: Zambrowicz, Brian
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and TITLE OF INVENTION: Polynucleotides Encoding the Same FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/09/733,388
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 3
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       gHisHisLeuHisProValSerAla***AspGlyGlnGlyProGlnThrValProAlaAr 326
                                                        GATCCTCAAGGCGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCCGACTCTGC
                                                                                                                                                      yLeuThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrTh
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US-09-733-388-1
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APPLICANT: Abuin, Alejandro
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6602698el Human Kinase Proteins
TITLE OF INVENTION: Polymucleotides Encoding the Same
FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/09/733,388
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
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TYPE: DNA
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                        LALaSerSerArgThrSer
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                                                          GAGTCCAAAATA-ATGATCAGTGACTTTGGATTGTCAAAAATGGAGGGCAAAGGAGATGT
                                                                                              n---ProAlaHisAlaLeuSerSerSerThrLeuAlaSerArgThrGlySerArgProVa
                                                                                                                                      ATGGGCATCGTCCACAGACCTCAAGCCCGAAAATCTCTTGTACTACAGTCAAGATGAG
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Turner, C. Alexander
Friedrich, Glenn
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APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and TITLE OF INVENTION: No. 6602698el Human Kinase Proteins and TITLE OF INVENTION: Polymucleotides Encoding the Same FILE REFERENCE: LEX-0103-USA
CURRENT APPLICATION NUMBER: US/09/733,388
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,428
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-733-388-5
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APPLICANT:
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ORGANISM: Homo
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Turner, C. Alexander Jr.
Friedrich, Glenn
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APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Wang, Yonghong
APPLICANT: Ma, Yunging
APPLICANT: Ma, Yunging
APPLICANT: Mang, Dinrui
APPLICANT: Mang, Dinrui
APPLICANT: Wang, Zhiwei
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6589662el Nucleic Aci.
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C172B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEO ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 526
LENGTH: 1733
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APPLICANT: Liu,
APPLICANT: Asund
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
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                                                                                              gHisHisLeuHisProValSerAla***AspGlyGlnGlyProGlnThrValProAlaAr 326
                                                                                                                              GATCCTCAAGGCGGAATATGAGTTTGACTCTCCCTACTGGGATGACATCTCCGACTCTGC
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RESULT 14 US-09-930-181-1 ; Sequence 1, Application US/09930181 ; Patent No. 6455292

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APPLICANT: Origene Technologies
APPLICANT: INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
TITLE OF INVENTION: Full-Length Serine Protein Kinase in Brain and Pancreas
FILE REFERENCE: 16U 101 V1
CURRENT PAPLICATION NUMBER: US/09/930,181
CURRENT FILING DATE: 2001-08-16
NUMBER OF SEQ ID NOS: 18
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LOCATION: (106)..(2112)
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oValAlaSerSerArgThrSerLeuAlaArgGlnSerSerSerValArgGlyArgCysGl
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                                          ----AGACCAGCTGTGGGTCCCCCCACTACGCCTGCCCCGAGGTGATCCGGGGGGAGAAG
                                                                   rMetGlnProAlaHisAlaLeuSerSerSerThrLeuAlaSerArgThrGlySerArgPr
                                                                                                ATCCGCATCGCAGACTTTGGCATGGCGTCCCTGCAGGTTGGCGACAGCCTGTTGG-----
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APPLICANT: Bird, Timothy A.
APPLICANT: Bird, Timothy A.
APPLICANT: Virca, G. Duke
APPLICANT: Martin, Unja
APPLICANT: Martin, Unja
APPLICANT: Martin, Unja
APPLICANT: Moderson, Dirk M.
APPLICANT: Anderson, Dirk M.
APPLICANTON OPEL MURINE AND HUMAN KINASES
FILE REFERENCE: 2923-A
CURRENT APPLICATION NUMBER: US/09/579,664B
CURRENT FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 36
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US-09-579-664B-3
                                                                                                                                                                                                                                                                                                                                  FIGURE9 (1-361) x US-09-579-664B-3 (1-1694)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09579664B Patent No. 6514719 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1023
                                                                                474
                                                                                                                                                                  426
                                                                                                                                                                                                     126 ArgArgGlyValSerArgGluGluIleGluArgGluValSerIleLeuArgGluIleArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1694
ATGCAACTTGTGTGTGGGGAGAACTCTTCGATCGGATAGTGGAGAAGGGGTTTTACACA
                          LeuGluLeuValSerGlyGlyGluLeuPheAspPheLeuAlaGluLys-AspHis***Gl
                                                                                                                                                                                                                                                                          LysGlyThrGlyMetGluTyrAlaAlaLysPheIleLysLysArgArgLeuProSerSer
                                                                             CATGAAAACATTGTTGCCTTGGAAGATATTATGAAAGCCCAAATCACCTCTACCTGGTC
                                                                                                                     HisProAsnIleIleThrLeuHisAspValPheGluAsnLysThrAspValValLeuIle 165
                                                                                                                                                                                                                                                  AAAGCTACTGGGAAGCTCTTCGCAGTGAAGTGCATCCCGAAGAAGGCGCCTGAAGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCACTCACTGG 1033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACACATATGGTATATAGGGGGCAAGAATGAGCCCGAACCAGAGCAGCCCATTCCTCGCAA
                                                                                                                                                             -----AAGGAGAGCAGCATCGAGAACGAGATTGCCGTGCTTAGAAAGATTAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YSLYSH1STrp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sHisLeuHisProValSerAla***AspGlyGlnGlyPro---GlnThrValPro----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTACGGGGCATGATCGAGGTGGACGCCGCACGCCTCACGCTAGAGCACATTCAGAA 902
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----Leu***ThrThrTrpLeuGlySer***TyrValGluHisArgArgHi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCTTG-CTGGTGGGGGCTCTGCCCTTCGACGATGACAACTTGCGACAGCTG----CTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus
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214.50
27.85%
47.85%
33.49%
11.75%
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Gaps:
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70
84
86
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	TGAACAGATCCTCAAGGCAGAATAT 956	932	B
	*ThrThrTrpLeuGlySer***Tyr 301	, 293	Š
931	ATCTTGCTCTGTGGTTACCCTCCTTTTTATGATGAAAATGACTCGAAGCTGTT 931	879	밁
293	273 yLeuGlyLeuThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu** 293		8
878	GAAACCGTACAGCAAAGCTGTGGACTGCTGGTCCATCGGGGTGATCGCCTAT	827	뮍
273	gGlnSerSerValArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGl	253	Ş
826	767 AGATGTGATGTCCACGGCCTGCGGGACCCCAGGCTATGTTGCTCCGGAAGTTCTCGCCCA 826		뮍
253	gProValAlaSerSerArgThrSer	242	Ş
766	708 GACGAGGAGTCCAAAATA-ATGATCAGTGACTTTGGCTTGTCGAAAAATGGAGGCAAAGG 766		B
242	nProAlaHisAlaLeuSerSerSerThrLeuAlaSerArgThrGlySerAr	. 225	Ş
707	654 ATGGGCATTGTCCACAGGGACCTCAAGCCGGAGAATCTCTTATACTACAGTCAA 707		В
225	oSerAlaSerArgThrLeuThr***SerArgArgThrSerCysCysTrpThrSerMetGl	205	8
653	GAGAAAGATGCCAGCACTCTCATCCGCCAGGTCCTGGATGCCGTATACTATCTCCACAGA 653	594	В
205		185	Ş

Search completed: July 1, 2004, 01:56:09 Job time: 185 secs

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GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Hanzel, David R.

APPLICANT: Hanzel, David K.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUTITLE OF INVENTION: EXPRESSION ANALYSIS TWO

FILE REFERENCE: AEOMICA-X-2

CURRENT APPLICATION NUMBER: US/10/029,386

CURRENT FILING DATE: 2001-12-20

NUMBER OF SEQ ID NOS: 34288

SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

SEQ ID NO 23553

LENGTH: 147
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                                                                                                                 RESULT 30
US-09-864-761-11330
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Best Local S
Matches 20
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SEQ ID NO 1
SENGTH: 157875
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 23553, Application US/10029386 Publication No. US20030194704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
Sequence 11330, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
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APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: NEUROPSYCHIATRIC
TITLE OF INVENTION: DISGADERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/04702 US0
CURRENT APPLICATION NUMBER: US/10/125,835
CURRENT FILING DATE: 2002-04-19
PRIOR APPLICATION NUMBER: US/09/757,300
PRIOR APPLICATION DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO CHR15.3

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2

OTHER INFORMATION: EXTRUMAN HIT: AA858002.1, EVALUE 3.00e-65

OTHER INFORMATION: SMISSPROT HIT: P53335, EVALUE 5.00e-18

OTHER INFORMATION: NT HIT: gi14670382, EVALUE 8.00e-77
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nes 21; Conservative (
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                                                                                                                                                                                                                                                                                                                 1.8%; Score 20; DB 15; Length 147; 100.0%; Pred. No. 7.1; tive 0; Mismatches 0; Indels
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APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENEMERSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT FILING DATE: 2001-05-23
PRIOR PPLICATION NUMBER: US 60/180,312
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR PPLICATION NUMBER: US 60/207,456
PRIOR PPLICATION NUMBER: US 60/23,366
PRIOR PPLICATION NUMBER: US 60/23,366
PRIOR PPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR PRILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                    FEATURE:
OTHER INFORMATION: MAP TO AC003669.1
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.97
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.81
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN BANIN, SIGNAL = 0.57
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers.
SOFT ID NO 11330
LENGTH: 447
TYPE: DNA
                                                                                                                                          Matches
                                                                                                                                                                                                             Query Match
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284 TGATCTTGGAGCTGGTGTCC 303
                                                                      500 TGATCTTGGAGCTGGTGTCC 519
                                                                                                                                  similarity 100.0%; p
                                                                                                                                                                             Score 20;
Pred. No.
                                                                                                                                             Mismatches
                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                    Length 447
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RESULT 31 US-09-918-995-38039

Sequence 38039, Application US/09918995 Publication No. US20030073623A1 GENERAL INFORMATION:

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US-10-220-120-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/960,643
CURRENT FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Yoganathan, Thillainathan APPLICANT: Delaney, Allen TITLE OF INVENTION: CANK-X1 and its Uses FILE REFERENCE: KINE024
CURRENT APPLICATION NUMBER: US/10/220,120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 13
                                                                                         APPLICANT:
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NAME/KEY: CDS
LOCATION: (70)...
                                                                                                                                     PPLICANT:
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TYPE: DNA
ORGANISM: H. sapiens
                           PLICANT: HODGSON, David M.
PLICANT: LINCOLN, Stephen E.
PLICANT: JACKSON, Stuart
TLE OF INVENTION: MOLECULES FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                 YAP, Pierre E.
YU, Jimmy Y.
BRADLEY, Diana L.
BRATCHER, Shawn R.
                                                                                                       CHEN
                                                                                                                                                                                                                                                                                                                                                           DANIELS, Susan E.
DUFOUR, Gerard E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHALUP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/10220120
                                                                                                                                                                                                                                                                                                   HILLMAN, Jennifer L.
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DAHL, Christopher R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHANG, Simon C.
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                                                                                                                                                                                 WRIGHT,
                                                                                                                                                                                            STOCKDREHER, Theresa K.
DAFFO, Abel
                                                                                                                                                                                                                          ROSEN, Bruce H.
RUSSO, Frank D.
                                                                                                                                                                                                                                                                                                                  GREENAWALT, Lila B.
                                                                                                                                                                                                                                                                                                                                                                          DANIELS,
                                                                                                                                                                                                                                                       JU, Tommy F.
COSEBERRY, Ann M.
                                                                                                                                                                                                                                                                                     JONES,
                                                                                                                                                                                                                                                                                                                                                FLORES,
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                                                                                                      Wensheng
                                                                                                                                                                                                                                                                                                                              Willy T
                                                                                                                                                                                                                                                                                                                                                                                                                                      Steven A.
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                                                                                                                                                                                                                                                                                   Anissa L.
                                                                                         Howard
                                                                                                                                                                               Rachel J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Michael S.
                                                                                                                                                                                                                                                                                                                                              Vincent
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; Pred. No. 1.8;
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APPLICANT: Meyer, Joanne
APPLICANT: Merer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/11702 US1
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 90
SOFTWARE: PatentIn version 3.0
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US-09-935-464-1
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                                                            US-10-125-835-1
                                                                                  RESULT 28
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SOFTMARE: PERL Program
SEQ ID NO 29
LENGTH.
Sequence 1, Application US/10125835 Publication No. US20030092019A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application Publication No. US200300 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 1
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Best Local :
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Best Local (
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PRIOR FILING DATE: 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-24; 2000-02-17; 2000-02-12; 2000-02-16; 2000-02-16; 2000-05-15;
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PRIOR APPLICATION NU
                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
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NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No. US20040048253A1 LI:333138.2:2000MAY01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
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60/184,769; 60/184,768;
60/184,772; 60/185,213;
60/204,815; 60/203,785;
                                                                                                                                              142369 CATCGGCGTCATCACCTACAT 142389
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21; Conservative 0;
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Conservative 0;
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184,771; 60/184,813; 60/184,773; 60/184,776;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002-08-26
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[00.0%; Pred. No. 1.
[ve 0; Mismatches
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%; Pred. No. 1.4
0; Mismatches
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60/205,221;
60/204,226;
60/205,287;
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APPLICANT: Castle, Arthur
APPLICANT: Elashoff, Michael
APPLICANT: Elashoff, Michael
TITLE OF INVENTION: Molecular Toxicology Modeling
FILE REFERENCE: 44921-5089-US
CURRENT APPLICATION NUMBER: US/10/152,319A
CURRENT FILING DATE: 2002-05-22
PRIOR APPLICATION NUMBER: US 60/292,335
PRIOR APPLICATION NUMBER: US 60/297,523
PRIOR PILING DATE: 2001-06-13
PRIOR FILING DATE: 2001-06-13
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US-10-152-319A-1918
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/298,925
PRIOR FILLING DATE: 2001-06-19
PRIOR PELLING DATE: 2001-07-10
PRIOR PELLING DATE: 2001-07-10
PRIOR PELLING DATE: 2001-07-10
PRIOR PELLING DATE: 2001-07-10
PRIOR PELLICATION NUMBER: US 60/303,807
PRIOR PELLICATION NUMBER: US 60/303,808
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR APPLICATION NUMBER: US 60/315,047
PRIOR APPLICATION NUMBER: US 60/324,928
PRIOR PILLING DATE: 2001-09-28
PRIOR PILLING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: US 60/330,867
PRIOR PILLING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR PILLING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/330,462
PRIOR FILLING DATE: 2001-10-22
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                                                                                                                                                                       Remaining Prior Application data removed - See File Wrapper or PALM. NUMBER OF SEQ ID NOS: 2221
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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TYPE: DNA
ORGANISM: Homo sapiens
-10-125-835-2
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: DISORDERS SUCH AS SCHIZOPHRENIA
FILLE REFERENCE: 3322/047702 US0
CURRENT FILING DATE: 2002-04-19
FRIOR APPLICATION NUMBER: US/09/757,300
PRIOR PETILNG DATE: 2001-01-09
NUMBER OF SEQ ID NOS: 50
NUMBER OF SEQ ID NOS: 50
SOFTMARE: Patentin version 3.0
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OTHER INFORMATION: Genbank Accession No. NM_031573 10-152-319A-1918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mendrick, Donna
APPLICANT: Porter, Mark
APPLICANT: Johnson, Kory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PPLICANT: Johnson, Kory
PPLICANT: Higgs, Brandon
                                                                                  ORGANISM: Rattus norvegicus
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100.0%; Pred. No. 1.8;
ative 0; Mismatches 0; Indels (
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; SEQ ID NO 4
; LENGTH: 1738
; TYPE: DNA
; ORCANISM: Homo sapiens
US-09-935-464-4
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                                                                                                  US-10-125-835-4
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Best Local Sim
Matches 21;
                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Parker, Alexander
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND TREATING
TITLE OF INVENTION: NEUROPSYCHIATRIC
TITLE OF INVENTION: DISCROERS SUCH AS SCHIZOPHRENIA
FILE REFERENCE: 3322/0H702 US0
CURRENT APPLICATION NUMBER: US/002-04-19
PRIOR APPLICATION NUMBER: US/09/757,300
PRIOR APPLICATION NUMBER: US/09/757,300
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
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Best Local Similarity 100.0%; P
                                                                                                                                                              SEQ ID NO 4
LENGTH: 1738
                                 Query Match
Best Local |
           Matches
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CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US 09/757,300
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
PRIOR FILING DATE: 2001-01-09
                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: DISCREES SUCH AS SCHIZOPHRENIA
TITLE OF INVENTION: DISCREES SUCH AS SCHIZOPHRENIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.0
                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quence 4, Application US/09935464
blication No. US20030027153A1
Local 5.
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       Similarity 100.0%; I
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100.0%; Pred. No. 1.:
tive 0; Mismatches
         1.9%; Score 21; DB 15; Length 1738; 100.0%; Pred. No. 1.8; or Indels
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919 CATCGGCGTCATCACCTACAT 939

629 CATCGGCGTCATCACCTACAT 649

US-10-037-270-809

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; NAME/KEY: misc feature
; LOCATION: (1)...(2165)
; OTHER INFORMATION: n = a,t,c or g
US-10-037-270-809
                                                                                                                                                                                                                                                                                                               RESULT 23
US-10-117-722-809
                                                                                                                                                                                                                                                 Sequence 809, Application US/10117722 Publication No. US20030219744A1 GENERAL INFORMATION:
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SEQ ID NO 809
LENGTH: 2165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
APPLICANT: Asundi, Vinod APPLICANT: Asundi, Vinod APPLICANT: Zhang, Jie APPLICANT: Drmanac, Radoje T. APPLICANT: Drmanac, Radoje T. TITLE OF INVENTION: No. US20030219744A1el Nucleic Acids and TITLE OF INVENTION: Polypeptides
FILE REPERENCE: 784CIP2BCIP
CURRENT APPLICATION NUMBER: US/10/117,722
CURRENT APPLICATION NUMBER: US/10/117,722
PRIOR APPLICATION NUMBER: 09/620,312
PRIOR FILING DATE: 2000-07-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/037,270
CURRENT FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 09/525,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/486,725
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
                                                                                                                                                                                    APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tillinghast, John
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. US20030104529A1el Nucleic Acids and
TITLE OF INVENTION: Folypeptides
FILE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NERAL INFO.
NERAL INFO.
APPLICANT: Tang, 1.
APPLICANT: Liu, Chenghua
A4. Vinod
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (1)
                                                                                                                                                                                                                                                                                                                                                                                                885 CATCGGCGTCATCACCTACAT 905
                                                                                                                                                                                                                                                                                                                                                                                                                                        919 CATCGGCGTCATCACCTACAT 939
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Zhang, Jie
Ren, Pelyan
Chen, Rui-hong
I: Zhao, Qing A.
Thoman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhou, . - Ma, Yunqing
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Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang, Dunrui
Wang, Zhiwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xue, Aidong J.
Yang, Yonghong
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o. US20030104529A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 21; DB 15;
Pred. No. 1.8;
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RESULT 25

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CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: IB01/02237
PRIOR FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: 60/290,555
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: 60/233,999
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR APPLICATION NUMBER: 60/237,419
PRIOR APPLICATION NUMBER: 60/237,423
PRIOR APPLICATION NUMBER: 60/237,423
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SEQ ID NO 809
LENGTH: 2165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/10380235
Publication No. US20040072184A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: (1)..(1704)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(2165)
OTHER INFORMATION: n = a,t,c or g
                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1104
                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: 60/238,558
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Yoganathan, Thillainathan
APPLICANT: Delaney, Allen
TITLE OF INVENTION: CANCER ASSOCIATED PROTEIN KINASES AND
TITLE OF INVENTION: THEIR USES
FILE REFERENCE: KINE-024CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                      LENGTH: 2447
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                      FEATURE:
NAME/KEY: CDS
LOCATION: (70)...(1498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%;
                                                                                                       Local
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                                       919 CATCGGCGTCATCACCTACAT 939
681 CATCGGCGTCATCACCTACAT 701
                                                                               l Similarity 100.0%; F
21; Conservative 0;
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                                                                                                                            1.9%;
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                                                                                  Score 21; DB 12; pred. No. 1.8; O; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                              Length 2447;
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RESULT 37
US-09-918-995-10392
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US-10-425-114-5579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack B
APPLICANT: Tabaska, Jack E
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 5579
LENGTH: 2382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 976
LENGTH: 2055
TYPE: DNA
ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                  Sequence 10392, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local
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                                                                  TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES FILE REFERENCE: 20411-756 CURRENT APPLICATION NUMBER: US/09/918,995 CURRENT FILLING DATE: 2001-07-30 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR APPLICATION NUMBER: US/09/235,076 PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windo
EQ ID NO 10392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Clone ID: 700465007_FLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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nes 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                 989
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                    FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGGCGGCGAACTTTTCGAC 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%; Score 20; DB 13; llarity 100.0%; Pred. No. 6.1; Conservative 0; Mismatches (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Sequence 89093, Application US/10027632
Publication No. US20030204075A9
GENERAL INFORMATION:
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RESULT 38
US-10-027-632-89093/c
; Sequence 89093, Application US/10027632
; Publication No. US20020198371A1
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 2000-02-24

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-09-28

PRIOR APPLICATION NUMBER: US 60/167,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28
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                                                                                  Query Match
Best Local S
Matches 19
                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 89093
LENGTH: 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1) ... (456)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 456
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232
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  275
                                          223 CAGAGGCTGGGGTACAGAG 241
                                                                                    19;
                                                                                                        Similarity
CAGAGGCTGGGGTACAGAG 257
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                  1999-08-09
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100.0%; Pred. No.
                                                                                                    1.7%; Score 19;
100.0%; Pred. No.
                                                                                0;
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                                                                                    Mismatches
                                                                                                      DB 13;
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23;
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mag
TITLE OF INVENTION: Polymorphisms in the
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12

and Mapping of Single Nucleotide in the Human Genome

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APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON N
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 9853
LENGTH: 535
; Sequence 1835, Application US/10087192 ; Publication No. US20020182586A1 ; GENERAL INFORMATION:
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; LOCATION: (1)...(493)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-38039
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                                                               RESULT 33
US-10-087-192-1835
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Best Local Simi
Matches 20;
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Publication No. US20
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9853, Application US/10029386 Publication No. US20030194704A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILLE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/99/235,076
PRIOR PRIOR PRIOR APPLICATION NUMBER: US/99/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASESEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Hyseq, Inc.
                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: MAP TO CHR15.3
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.53
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.85
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.89
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.00e-111
OTHER INFORMATION: EST HUMAN HIT: A8658002.1, EVALUE 1.00e-123
OTHER INFORMATION: SWISSPROT HIT: PA53355, EVALUE 5.00e-30
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100.0%; Pred. No.
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6.7;
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US-10-425-114-25191
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US-10-087-192-1835
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US-10-425-114-976
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PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1835
LENGTH: 1716
                                                                                                  Sequence 976, Application US/10425114 Publication No. US20040034888A1 GENERAL INFORMATION:
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LENGTH: 1934
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Publication No. US20040034888A1
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Best Local
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Best Local (
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APPLICANT:
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APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yiham
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven B
APPLICANT: Tabaska, Jack E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
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APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, Dav
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APPLICANT: Engelhard, Eric K.
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Screen, Steven E
Tabaska, Jack E
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Yongwei

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FILE REFERENCE: 2041-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 313
LENGTH: 488
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US-09-918-995-313
; Sequence 313, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
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US-10-027-632-136289
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NUMBER OF SEQ ID NOS: 1140
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 230
LENGTH: 2287
TYPE: DNA
ORGANISM: Rattus norvegicus
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
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Matches
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Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129
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LOCATION: (1)...(488)
OTHER INFORMATION: n = A,T,C
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OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_031985
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100.0%; Pred. No.
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RESULT 14
US-10-027-632-136289
/ Sequence 136289, Application US/10027632
/ Publication No. US20030204075A9
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; SEQ ID NO 136289
; LENGTH: 692
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-136289
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-9
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-9
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/16,358
PRIOR PILING DATE: 1999-09-28
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US-10-027-632-136290
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Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                        Best
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PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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SOFTWARE: FastSEQ for
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Similarity 100.0%;
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100.0%; Pred. No.
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT PILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 12000-02-24
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 136290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
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                                                                                                                                                                                        ; ORGANISM: Human
US-10-027-632-136290
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US-10-027-632-136290
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Publication No. US20030204075A9 
GENERAL INFORMATION:
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Best Local Similarity
Matches 21; Conserv
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LENGTH: 692
                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Human
-10-027-632-136289
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                      LENGTH:
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                                                                                                                                                                                                                                                                   692
CATCGGCGTCATCACCTACAT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.9%; Score 21; DB ilarity 100.0%; Pred. No. 1.9 Conservative 0; Mismatches
                                                                              1.9%; Score 21; DB 16; Length 692; Larity 100.0%; Pred. No. 1.9; Conservative 0; Mismatches 0; Indels
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RESULT 18
US-10-125-835-2
; Sequence 2, Application US/10125835
; Publication No. US20030092019A1
; GENERAL INFORMATION:
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US-09-935-464-2
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Coldman, Barry S.
APPLICANT: Chen, xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF MICROBIAL PROTEINS IN PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(5202)B
FILE REFERENCE: 38-10(5202)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/86/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 42833
LENGTH: 1052
TWOPE: NUM
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Meyer, Joanne
APPLICANT: Meyer, Joanne
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Martin, Rory
APPLICANT: Barrington-Marinor
APPLICANT: PILE REFERENCE: 3322/1H702 US1
FILE REFERENCE: 302/1008-23
CURRENT APPLICATION NUMBER: US/09/935,464
CURRENT FILING DATE: 2001-08-23
PRIOR APPLICATION NUMBER: US/09/757,300
PRIOR FILING DATE: 2001-01-09
NUMBER OF EGG ID NOS: 90
SOFTWARE: Patentin version 3.0
SEQ ID NOS: 90
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Publication No. US20030027153A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 21; Conserv
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1383
TYPE: DNA
ORGANISM: Homo sapiens
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                                                                                                                                                                                                       919 CATCGGCGTCATCACCTACAT 939
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Pred. No.
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TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REFERENCE: 38-21(53313)B
CURRENT APPLICATION NUMBER: US/10/425,114
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 73128
SEQ ID NO 16427
LENGTH: 1467
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
1.7%; Score 19; DB 13; Length 1467;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 0; Indels (
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1.7%; Score 19; DB 15; Length 1640;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 19; Conservative 0; Mismatches 0; Indels
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Sequence 25, Application US/10210120

Publication No. US20030175736A1

GENERAL INFORMATION:
APPLICANT: Chinnaiyan, Arul M.
APPLICANT: Rubin, Mark A.

TITLE OF INVENTION: Expression Profile of Prostate Cancer;
FILE REFRENCE: UN-07221

CURRENT APPLICATION NUMBER: US/10/210,120

CURRENT APPLICATION NUMBER: US 60/309,581

PRIOR APPLICATION NUMBER: US 60/309,581

PRIOR APPLICATION NUMBER: US 60/304,468

PRIOR APPLICATION NUMBER: US 60/334,468

PRIOR FILING DATE: 2001-01-15
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| NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20030119009A1 471362.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 18, Application US/10084817
| Publication No. US20030119009A1
| GENERAL INFORMATION:
| APPLICANT: Suan Stuart
| APPLICANT: Jed G. Nuchtern
| FILE REFERENCE: PA-0046 US
| CURRENT APPLICATION NUMBER: 60/270,784
| PRIOR APPLICATION NUMBER: 60/270,784
| PRIOR FILING DATE: 2001-02-23
| NUMBER OF SEQ ID NOS: 365
| SOFTWARE: PERL Program
| SEQ ID NO 78
| LENGTH: 1640
| TYPE: DNA
| ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Clone ID: LIB3064-097-F3_FLI
US-10-425-114-16427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         648 AAGCCGGAGAACATCATGT 666
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                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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SOFTWARE: PatentIn version 3.1
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FGRENEULC, RODGEL
APPLICANT: TAUMENTON, RODGEL
APPLICANT: Xu, H.
TITLE REPERBACE: ELITRA,034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PLING DATE: 2000-05-26
PRIOR PLING DATE: 2000-05-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-09-09
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/25,931
PRIOR PLING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PLING DATE: 2001-02-09
PRIOR PRILING DATE: 2001-02-09
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1.7%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches
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Publication No. US2004003488A1
GENERAL INFORMATION:
APPLICANT: Liu, Jingdong
APPLICANT: Zhou, Yihua
APPLICANT: Kovalic, David K.
APPLICANT: Screen, Steven E
APPLICANT: Tabaska, Jack E
                                                                                                                          Sequence 33150, Application US/10282122A Publication No. US20040029129A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                 APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Pseudomonas syringae
                                                                                                                                                                                                                                                                                                                                                                                                                    Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
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US-10-425-114-16427
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APPLICANT: Budworth, Paul R.
APPLICANT: Budworth, Steven P.
APPLICANT: Cooper, Steven P.
APPLICANT: Cooper, Steven P.
APPLICANT: Glazebrook, Jane
APPLICANT: Gradiati, Fumiyaki
APPLICANT: Karagiati, Fumiyaki
APPLICANT: Ricke, Darrell
APPLICANT: Provart. Nicholas
APPLICANT: PLOVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION
FILE REFERENCE: 60111-NP
FILE REFERENCE: 60111-NP
FILE REFERENCE: 60111-NP
FILE REPERENCE: 60111-NP
FRIOR PELLING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR PELING DATE: 2001-09-26
PRIOR FILING DATE: 2001-09-26
PRIOR FILING DATE: 2002-04-04
NUMBER OF SEQ ID NOS: 6077
SEQ ID NO SEQ ID NOS: 6077
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100.0%; Pred. No. 23;
ive 0; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.8
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.3
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 4.7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.0
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.0
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 2.6
OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 3.0
US-09-864-761-8409
             PRIOR FILING DATE: 2000-09-21
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 8409
LENGTH: 559
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100.0%; Pred. No. 22;
ive 0; Mismatches
   PRIOR APPLICATION NUMBER: US 60/234,687
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Publication No. US20040016025A1
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Best Local Similarity 100.0
Matches 19; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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JS-10-260-238-160
                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
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Patent No. US20020048763A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Rank, David R.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David R.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR PLICATION NUMBER: US 60/180,312
PRIOR APPLICATION NUMBER: US 60/180,312
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1.7%; Score 19; DB 16; Length 504;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 19; Conservative 0; Mismatches 0; Indels
PRIOR APPLICATION NUMBER: US 60/198, b.o.
PRIOR FILING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-03-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SEQ ID NO 89093
LENGTH: 504
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PRIOR PELLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-06-03
PRIOR PILLING DATE: 2000-06-03
PRIOR PILLING DATE: 2000-06-03
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2000-10-04
PRIOR PILLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PILLING DATE: 2001-01-30
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PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
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ORGANISM: Human
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Maximum DB
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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/ cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/ cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
/ cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
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US-10-083-641A-6
US-09-908-975-3053
US-10-087-192-1832
US-10-087-192-1831
US-10-087-192-1831
US-10-087-192-1834
US-10-316-253-31
US-10-316-253-33
US-10-191-803-230
US-09-918-995-313
US-09-918-995-313
US-10-027-632-136289
US-10-027-632-136289
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ibpna/PCT_NEW_PUB.seq:*
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9340.072 Million cell updates/sec
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                                           Sequence 6, Appli
Sequence 3053, Ap
Sequence 1182, Ap
Sequence 118, Appl
Sequence 11, Appl
Sequence 1834, Ap
Sequence 1834, Ap
Sequence 31, Appl
Sequence 31, Appl
Sequence 31, Appl
Sequence 313, Appl
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US-10-083-641A-6

Sequence 6, Application US/10083641A Publication No. US20030017568A1 GENERAL INFORMATION:

APPLICANT: HAYSTEAD, TIMOTHY A
TITLE OF INVENTION: SMOOTH MUSCLE MYOSIN PHOSPHATASE ASSOCIATED KINASE
FILE REFERENCE: 1579-647

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-10-210-120-2	-10-084-817-7	0-425-114-1642	-10-282-122A-3	-10-260-238-16	9-864-761-840	S-10-027-632-8909	-10-027-632-890	-09-918-995-1039	5-114-557	-10-425-114-97	-10-425-114-251	-10-087-192-183	-10-029-386-985	-09-918-995-38	09-864-761-1133	S-10-029-386-235	-10-125-835-	-09-935-464-	-10-220-120-	-09-960-643-	-10-380-235-	-10-117-722-80	0-037-270-8	-10-125-835-	-09-935-464-	0-152-319A	-10-125-835-	-09-935-464-	-10-369-493-4283	7-632-136	
quence 25	equence 78, Ap	equence 164	е 33150,	equence 160, Ap	quence 8409, A	equence 89093,	e 89093,	equence 10392,	e 5579	equence 976, 1	equence 25191,	equence 18	equence 9853,	equence 38	quence 113	nce 235	equence 1,	equence 1,	equence 29,	equence 1,	nce 3,	equence 809	equence 8	Ф ,4 ,	equence 4,	equence 191	equence 2,	nce 2,	quence 428	equence 1362	

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## ALIGNMENTS

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SEQ ID NO 6
LENGTH: 1093
                                                                                                                                     Query Match
Best Local Similarity
Matches 1093; Conserv
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CURRENT FILING DATE: 2002-02-27
PRIOR APPLICATION NUMBER: 60/271,436
PRIOR FILING DATE: 2001-02-27
NUMBER OF SEQ ID NOS: 17
                                                                                                                                                                                                            FEATURE:
NAME/KEY: Unsure
LOCATION: (2), (7), (37), (39), (1056), (1081) and (1092)
OTHER INFORMATION: N can be A, C, G or T
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Putative nucleotide OTHER INFORMATION: sequence of smooth muscle MYPT-Kinase
GACCTCCTTCTTTCTCGCCCCCAGCACGGGATTAACCTCACTTGACTGTTCTTGGGTCCC
                                                         GNTATGNATATCGGTTTAATCGGCCGGAGCTCGCCCNCNGGGCAGCTGGACTCCCTCTCA
                                                                                                GNTATGNATATCGGTTTAATCGGCCGGAGCTCGCCCNCNGGGCAGCTGGACTCCCTCTCA
                                                                                                                                   100.0%; Silarity 100.0%; For Conservative 0;
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Pred. No. 0;
0; Mismatches
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RESULT 4
US-10-262-445-118
(S-10-262-445-118); Sequence 118, Application US/10262445; Publication No. US20040014058A1; GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John
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RESULT 2 US-09-908-975-3053

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Sequence 3053, Application US/09908975

Publication No. US20030165843A1

GENERAL INFORMATION:
APPLICANT: HOSHAN, Avi
APPLICANT: HASSERMAN, Alon
APPLICANT: MINTZ, Liat
APPLICANT: MINTZ, Liat
APPLICANT: FAIGLER, Simchon
TITLE OF INVENTION: CLICONUCLECTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLICE V
TITLE OF INVENTION: THAT POPULATE A TRANSCRIPTOME
TITLE OF INVENTION UNMEER: US/09/908,975
CCURRENT APPLICATION NUMBER: US/09/908,975
CCURRENT APPLICATION NUMBER: US/09/908,975
CCURRENT APPLICATION NUMBER: US/09/287,724
PRIOR APPLICATION UNMEER: US 60/287,724
                                                                                                                                                                                                                                                                                                                                                      APPLICANT ENGELIARD, ETIC K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND M.
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1832
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TYPE: DNA
; ORGANISM: Rattus norvegicus
US-09-908-975-3053
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                                                                                                                                                                                                                                                                   ; ORGANISM: Mus musculus US-10-087-192-1832
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APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric
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Best Local :
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Matches :
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                                       445 CACCCCAACATCATCACGCTGCACGA 470
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l Similarity 100.0%;
44; Conservative
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                                                                                                                                     l Similarity
26; Conser
   CACCCCAACATCATCACGCTGCACGA
                                                                                                                                 2.4%; Score 26; DB 13;
larity 100.0%; Pred. No. 0.0039;
Conservative 0; Mismatches 0;
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US-10-316-253-31

NAME/KEY: CDS LOCATION: (134)...( OTHER INFORMATION:

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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
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Sequence 31, Application US/10316253
Publication No. US20030162706A1
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LCCATION: (1)...(152330)
OTHER INFORMATION: n = A,T,C or G
:-10-087-192-1834
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Publication No. US20020182586A1
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                                                              TITLE OF INVENTION: Anglogenesis Modulating Proteins FILE REFERENCE: 8865M CURRENT APPLICATION NUMBER: US/10/316,253 CURRENT FILING DATE: 2002-12-10 PRIOR APPLICATION NUMBER: US 60/355,295 PRIOR FILING DATE: 2002-02-08 UNMBER OF SEQ ID NOS: 308 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:

APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Morris, David W. APPLICANT: Engelhard, Eric K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-087-192-1834
TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
                                                   LENGTH: 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH: 152330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120680 GGCGTCATCACCTACATCCTGTGAGT 120705
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26; Conservative
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                                                                                                                                                                                                                                                                  Greis, Kenneth
                                                                                                                                                                                                                                                                                                          Thompson, Larry
                                                                                                                                                                                                                                                                                       Feng
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100.0%; Pred. No. 0.003;
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                                                                               Query Match
Best Local
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                                                                                                                                                                                                                                                                                         FILE REFERENCE: 8865M
CURRENT APPLICATION NUMBER: US/10/316,253
CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 60/355,295
PRIOR FILING DATE:/2002-02-08
NUMBER OF SEQ ID NOS: 308
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: The Procter & Gamble Company
APPLICANT: Peters, Kevin
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TITLE OF INVENTION: Angiogenesis Modulating Proteins
                                                                                                                                           NAME/KEY: CDS
LOCATION: (22)..(1
OTHER INFORMATION:
                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                           TYPE: DNA ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                            ENGTH: 2287
                                                              Local Similarity 100. es 24; Conservative
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673 GACCTGAAGCCGGAGAACATCATG 696
                               642 GACCTGAAGCCGGAGAACATCATG 665
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                                                        100.0%; **
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b; Pred. No. 0.0
0; Mismatches
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; Pred. No. 0.045;
                                                                           DB 15;
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APPLICANT: HIGGS, Brandon
APPLICANT: CASTLE, Arthur
APPLICANT: CASTLE, Arthur
APPLICANT: ELASHOFF, Michael
TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
FILE REFERENCE: 44921-5090US
CURRENT APPLICATION NUMBER: US/10/191,803
CURRENT FILING DATE: 2002-07-10
PRIOR APPLICATION NUMBER: US 60/303,819
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR APPLICATION NUMBER: US 60/305,623
PRIOR FILING DATE: 2001-07-17
PRIOR FILING DATE: 2002-04-03
PRIOR FILING DATE: 2002-04-03
PRIOR APPLICATION NUMBER: US 60/369,351
PRIOR APPLICATION NUMBER: US 60/377,611

US-10-191-803-230

Sequence 230, Application US/10 Publication No. US20040014040A1

US/10191803

GENERAL INFORMATION:

APPLICANT: MENDRICK, Donna APPLICANT: PORTER, Mark

JOHNSON, Kory

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ORGANISM: Homo sapiens FEATURE:
NAME/KEY: CDS
LOCATION: (94)..(1455)
US-10-262-445-118
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US-10-059-585-11
Sequence 11, Application US/100
Publication No. US20030082776A1
GENERAL INFORMATION:
APPLICANT: Ota, Toshio
APPLICANT: Isogai, Takao
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 118
LENGTH: 2132
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                                                                                                                                                                                                                                                                                        Query Match
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CURRENT APPLICATION NUMBER: US/10/262,445
CURRENT FILING DATE: 2002-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2001-10-05
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-09
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NUMBER OF SEQ ID NOS: 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/327,454
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                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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OR FILING DATE: 2001-10-09
OR APPLICATION NUMBER: 60/328,056
OR FILING DATE: 2001-10-09
OR APPLICATION NUMBER: 60/328,849
OR APPLICATION NUMBER: 60/329,414
OR FILING DATE: 2001-10-15
OR FILING DATE: 2001-10-15
OR FILING DATE: 2001-10-15
                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 2001-10-17
APPLICATION NUMBER: 60/341,058
FILING DATE: 2001-10-22
APPLICATION NUMBER: 60/343,629
FILING DATE: 2001-10-24
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                                                                                                                                                                              445
                                                                                                                                                                                                                                                       26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND METHODS INVENTION: THE SAME
                                                                                                                                                                                CAGTTCCTCAAGCAGATCCTGGACGG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zerhusen, Bryan
Zhong, Haihong
Zhong, Mei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rieger, Danier
Spytek, Kimberly
Taupier Jr., Raymond J.
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                                                                         Application US/10059585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patturajan, Meera
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                                                                                                                                                                                                                                                     2.4%; Score 26; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
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Xiaojia
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                                                                                                                                                                                                                                                                            Score 26; DB 16; pred. No. 0.0038;
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APPLICANT: OLBUKİ, TetBUJİ
APPLICANT: FUNALSHİ, SHİN-ICHİ
APPLICANT: Senoo, Chiaki
APPLICANT: Nezu, Jun-IChİ
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN
TITLE OF INVENTION: KINASE/PROTEIN PHOSPHATASE
FILE REFERENCE: 06501-098001
CURRENT APPLICATION NUMBER: US/10/059,585
CURRENT FILING DATE: 2002-01-29
PRIOR APPLICATION NUMBER: PCT/JP00/05060
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,322
PRIOR APPLICATION NUMBER: US 60/183,326
PRIOR APPLICATION NUMBER: US 60/183,326
PRIOR APPLICATION NUMBER: US 60/183,327
PRIOR APPLICATION NUMBER: US 60/183,326
PRIOR APPLICATION NUMBER: US 60/183,326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-087-192-1831, Application US/10087192; Sequence 1831, Application US/10087192; Publication No. US20020182586A1; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 11
                                                                                                      NUMBER OF SEQ ID NOS: 2059
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1831
LENGTH: 126413
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APPLICANT:
APPLICANT:
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TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (215)...(1576)
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APPLICANT:
APPLICANT:
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PRIOR FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: JP 2000-183767
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: JP 11-248036
                                                                                                                                                                                                     APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-13-02
PRIOR FILING DATE: 2001-03-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-07-29
NAME/KEY: misc_feature
                                               TYPE: DNA ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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Otsuki, Tetsuj
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Wakamatsu, Ai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yamamoto, Jun-ichi
Ishii, Shizuko
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Otsuka, Kaoru
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Result
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Maximum DB
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Perfect score:
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| CGD2_6/ptodata/2/ina/6A_COMB.seq:*
| CGD2_6/ptodata/2/ina/6B_COMB.seq:*
| CGD2_6/ptodata/2/ina/6B_COMB.seq:*
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## ALIGNMENTS

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Sequence 4, Application US/09186277

| Retent No. 6171841
| GENERAL INFORMATION:
| APPLICANT: KAIRA, SHIZUO
| APPLICANT: KAWAI, TARO
| TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
| FILE REFERENCE: 081356/0128
| CURRENT APPLICATION NUMBER: US/09/186,277
| CURRENT FILING DATE: 1998-11-05
| EARLIER APPLICATION NUMBER: UJ97/261589
| EARLIER APPLICATION NUMBER: UJ97/261589
| EARLIER APPLICATION NUMBER: UJ97/261589
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| EARLIER APPLICATION NUMBER: UJ97/261589
| EARLIER APPLICATION NUMBER: UJ97/261589
| EARLIER APPLICATION DATE: 1997-09-26
| SOFTWARE: Patentin Ver. 2.0
| SEQ ID NO 4
| LENGTH: 1429
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; LOCATION: (10
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APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: pH-569
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER APPLICATION NUMBER: JP97/261589
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 4
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Matches 44; Conserv
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TYPE: DNA
ORGANISM: Mus
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Sequence 3, Application US/09186277

Patent No. 6171841

GENERAL INFORMATION:
APPLICANT: AKIRA, SHIZUO
APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: 081356/0128

CURRENT APPLICATION NUMBER: US/09/186,277

CURRENT FILING DATE: 1998-11-05

EARLIER APPLICATION NUMBER: UP97/261589

EARLIER APPLICATION DATE: 1997-09-26

NUMBER OF SEQ ID NOS: 8

SOFTWARE: Patentin Ver. 2.0
; NAME/KEY: CDS
; LOCATION: (94)..(1455)
US-09-186-277-3
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                                                                                                                          SEQ ID NO 3
LENGTH: 2132
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SEQ ID NO 3
LEUGTH: 2132
TYPE: DNA
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Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 44; Conservative 0; Mismatches 0;
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APPLICANT: KAWAI, TARO
TITLE OF INVENTION: DNA CODING FOR SERINE/THREONINE KINASE
FILE REFERENCE: PH-569
CURRENT APPLICATION NUMBER: US/09/159,385
CURRENT FILING DATE: 1998-09-23
EARLIER FILING DATE: 1997-09-26
EARLIER FILING DATE: 1997-09-26
NUMBER OF SEQ ID NOS: 8
                                                            TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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LOCATION: (94)..(1455)
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LOCATION: (10)..(1353)
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ORGANISM: Mus musculus
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APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Mang, Yunqing
APPLICANT: Mang, Zunqing
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Zhiwei
APPLICANT: Urmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569672el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILLS REPERENCE: 784C1P2B
FILLS REPERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT APPLICATION NUMBER: 09/952,317
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION DATE: 2000-01-21
NUMBER DATE: 2000-01-21
                                                                                                                                          US-09-313-294A-6448
                                                                                                                                                               RESULT 6
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                                                                             Sequence 6448, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt_FL_genes Version 1.0
SEQ ID NO 809
LENGTH: 2165
TYPE: DNA
ORGANISM: Homo sapiens
                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                       Query Match
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Best Local Similarity 100.0%; Pred. No. 0.0019;
Matches 26; Conservative 0; Mismatches 0;
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Patent No. 65696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Tang, Y. 10m
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Lalgudi, Raghunath V. APPLICANT: Ito, Laura Y. APPLICANT: Sherman, Bradley K. TITLE OF INVENTION: POLYNUCLEOTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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NAME/KEY: CDS
LOCATION: (1)..(1704)
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                                                                                                                                                                                                                                                                                                 Local Similarity 100.0%; nes 21; Conservative
                                                                                                                                                                                                                          885 CATCGGCGTCATCACCTACAT 905
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Zhang, Jie
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  POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
                                                                                                                                                                                                                                                                                                                        1.9%; Score 21; DB 4; L00.0%; Pred. No. 0.69;
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                                                                                                                                                                                                                                                                                                                                           Length 2165;
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FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6448
LENGTH: 295
TYPE: DNA
TYPE: DNA
CRGANISM: Zea mays
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US-08-510-878-3
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                                                                        US-08-510-878-3
                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 22040-0747
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
**DDITCATION NUMBER: US/08/510,878
                                                                                                                                                                                                                             NAME: Weiner, Marc S
REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 1254
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 205-8050
TELEPAX: (703) 205-8050
INFORMATION FOR SEQ. ID NO: 3:
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Query Match 1.8%; Score 20; DB 1; Best Local Similarity 100.0%; Pred. No. 2.2; Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700351821H1
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                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/00
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: KATO, MAMI
TITLE OF INVENTION: A KANAMYCIN RESISTANCE GENE DERIVED FROM
TITLE OF INVENTION: MICROORGANISMS OF THE GENUS RHODOCOCCUS
                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 3
                                                                                         HYPOTHETICAL:
ANTI-SENSE: 1
                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Birch, St. STREET: P.O. Box 747 CITY: Falls Church
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                         LENGTH: 748 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                            TOPOLOGY:
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Pred. No.
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 4554

LENGTH: 67-2
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                                                                                      RESULT 10
US-09-252-991A-4449/c
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Best Local S
Matches 20
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Patent No. 6346606
GENERAL INFORMATION:
APPLICANT: Marc J.
TITLE OF INVENTION:
                                                     Sequence 4449, Application Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity
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TITLE OF INVENTION: Protein Containing an SRCR Domain
FILE REFERENCE: 4121-108
CURRENT APPLICATION NUMBER: "US/09/341,587
CURRENT FILING DATE: 1999-08-31
EARLIER APPLICATION NUMBER: PCT/DE98/00096
EARLIER FILING DATE: 1998-01-09
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
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TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Pseudomonas aeruginosa
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20; Conservative
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 Rubenfield et al.

NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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100.0%; Pred. No.
tive 0; Mismatci
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00.0%; Pred. No.
                                                                           US/09252991A
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US-09-394-455-14
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APPLICANT: Witman, George F.
APPLICANT: San Agustin, Jovenal
APPLICANT: Leszyk, John D.
TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
FILE REFERENCE: 07911/078001
CURRENT APPLICATION NUMBER: US/09/394,455
CURRENT APPLICATION NUMBER: US 60/099,771
PRIOR APPLICATION NUMBER: US 60/099,771
PRIOR FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 56
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 4158
LENGTH: 1347
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                                                                                                                                                                                                                                                                                                        Sequence 14, Application US/09394455 Patent No. 6531305
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Patent No. 6551795
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LENGTH: 1335
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION 1998-02-18
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACII
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR TILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Pseudomonas aeruginosa
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18; Conserv
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1 Similarity 100.0%; F
18; Conservative 0;
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1998-02-18
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NUCLEIC ACID AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
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100.0%; Pred. No.
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%; Pred. No. 23;
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US-09-409-604-1
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; LOCATION: (30)...(1058)
US-09-394-455-14
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Best Local Similarity
Matches 18; Conserva
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SEQ ID NO 1
                                                                                                                                                                                                                                                                                  Sequence 155, Application US/09980052 Patent No. 6670130 GENERAL INFORMATION:
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GENERAL INF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 18; Conserv
           PRIOR APPLICATION NUMBER: KR 10-1999-0019631
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: KR 10-1999-0019632
PRIOR FILING DATE: 1999-05-29
PRIOR APPLICATION NUMBER: KR 10-1999-0019633
PRIOR FILING DATE: 1999-05-29
PRIOR PRIOR DATE: 1999-05-29
PRIOR PRIOR DATE: 1999-05-29
PRIOR FILING DATE: 1999-05-29
                                                                                                                                                      APPLICANT: KIM, Jeong Joon; SJ HIGHTECH Co., Ltd.
APPLICANT: KIM, Cheol Min
APPLICANT: PARK, Hee Kyung
TITLE OF INVENTION: Oligonucleotide for detection and identification of Mycobacteria
FILE REFERENCE: PP05020/PCT
CURRENT APPLICATION NUMBER: US/09/980,052
CURRENT FILING DATE: 2001-11-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: UTSD:573
CURRENT APPLICATION NUMBER: US/09/409,604A
CURRENT FILING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Watson, Mark L.
APPLICANT: Inoue, No. 6632934imitsu
APPLICANT: Hess, Karl D.
APPLICANT: Albright, George M.
APPLICANT: Albright, George M.
TITLE OF INVENTION: MORC GENE COMPOSITIONS AND METHODS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
LOCATION: (10)
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KR 10-1999-0019635
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PRIOR APPLICATION NUMBER: KR 10-2000-0018189
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 243
SOFTWARE: Kopatentin 1.71
SEQ ID NO 155
LENGTH: 20
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Best Local
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                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1941:
                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                         NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 02354
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...261
SEQUENCE DESCRIPTION: SEQ ID NO: 1941:
                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE
                                                                                                                                            TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                       FEATURE:
                                                                                                                           HYPOTHETICAL: NO
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17; Conserv
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OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                     TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: ASCII
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                                                                         ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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100.0%; P7
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Dumas Milne Edwards,
APPLICANT: Jobert, S.
APPLICANT: Jobert, S.
APPLICANT: Jobert, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 8505
LENGTH: 375
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                                                                                                     US-09-252-991A-8200
                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8200
LENGTH: 411
                                 Query Match
Best Local S
Matches 17
                                                                                                                                                                                                                                                                                                                                                                     Sequence 8200, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                               FILE REFERENCE: 107196.136
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
CURRENT FILING NUMBER: US 60/074,788
                                                                                                                                                                                                                                                                                                        APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
LOCATION: 333,344,348
OTHER INFORMATION: n=a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                    ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                      TYPE: DNA
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                                   l Similarity 100
17; Conservative
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CGGCCAGTTCGCCATCG 307
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                                                                     Length 411;
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342 CGGCCAGTTCGCCATCG 326

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APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Giordano, J.Y.
APPLICANT: Giordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 2248
LENGTH: 467
TYPE: DNA
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US-09-22-991A-13127/c
(Sequence 13127, Application US/09252991A
; Sequence 13127, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: APPLICANT AND THERAPEUTICS
                                                                                                           RESULT 20
US-08-797-812-25
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                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-13127
                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 13127
LENGTH: 507
TYPE: FOR
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                                                       Sequence 25, Application US/08797812 Patent No. 6228575 GENERAL INFORMATION:
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Best Local
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Patent No. 6639063
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 129.,446
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                                      APPLICANT:
         APPLICANT:
                        APPLICANT:
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Gingeras, Thomas A.
Mack, David
Chee, Mark S.
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100.0%; Pred. No.
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RESULT 21
US-09-252-991A-11363
US-09-252-991A-11363, Application US/09252991A
; Sequence 11363, Application US/09252991A
; Patent No. 6551795
; Patent No. 6551795
; FALENT NORMATION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TITLE OF INVENTION: ARROGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 199-02-18
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REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 1652
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
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Best Local Similarity
Matches 17; Conserv
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PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
ETLING DATE: 01-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 60/011,339
FILING DATE: 08-FEB-1996
ATTORNEY/ACENT INFORMATION:
NAME: Pitts Renea A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Chip-Based Species Identification and TITLE OF INVENTION: Phenotypic Characterization of Microorganisms NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: C
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                                                                                                                                                                                                                                                                                                                                         663
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Stryer, Lubert
Ghandour, Ghassan
Wang, Ching
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GENERAL INFORMATION:

APPLICATI: MATC J. Rubenfield et al.

APPLICATI: MATC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO I

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107195.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 11343

LENGTH: 930
                                                                                                                   APPLICANT: MARC J. Rubenfield et al.
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES REL.
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTIC
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US-60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
INUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2244
TYPE: DNA
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US-09-252-991A-2244/c
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GENERAL INFORMATION:
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Patent No. 6551795
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Query Match
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                                                                                 TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
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Score 17;
Pred. No.
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  DB 4;
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; SEQ ID NO 11960
; LENGTH: 993
; TYPE DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-11960
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US-09-252-991A-11960/c
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                                                                                                                                                                                                                              APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 2600
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Patent No. 6551795
                                                                                           Query Match
Best Local (
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Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                         LENGTH: 999
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
723 CGGCCAGTTCGCCATCG 739
                                    291 CGGCCAGTTCGCCATCG 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          588 TGCACGGCCTTGGCCTG 572
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17; Conservative 0; Michael 17;
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                                                                          Conservative 0;
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                                                                                             1.6%; Score 17;
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                                                                                                                DB 4; Length 999;
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RESULT 26 US-09-252-991A-8255

Sequence 8255, Application US/09252991A Patent No. 6551795

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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8255
LENGTH: 999
TYPE: FNA
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8255
                                                                                                                                                                                       RESULT 28
US-09-252-991A-12024
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US-09-394-455-3
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Sequence 12024, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 17; Conserv
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SEQ ID NO 3
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Best Local
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CURRENT APPLICATION NUMBER: US/09/394,455
CURRENT FILING DATE: 199-09-10
PRIOR APPLICATION NUMBER: US 60/099,771
PRIOR FILING DATE: 1998-09-10
NUMBER OF SEQ ID NOS: 56
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TITLE OF INVENTION: SPERM ASSOCIATED PROTEIN KINASE POLYPEPTIDES,
TITLE OF INVENTION: NUCLEIC ACIDS, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BENERAL INFORMATION:
APPLICANT: Witman, George F.
APPLICANT: San Agustin, Jove:
APPLICANT: Leszyk, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (1)...(1008)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH: 1008
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100.0%; Pred. No.
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Pred. No.
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US-09-252-991A-2312/c
/ Sequence 2312, Application US/09252991A
/ Patent No. 6551795
; ORGANISM: Pseudomonas aeruginosa US-09-252-991A-11990
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LENGTH: 1095
TYPE: DNA
                                                            SEQ ID NO 11990
LENGTH: 1119
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SEQ ID NO 12024
LENGTH: 1014
TYPE: DNA
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GENERAL INFORMATION:
                                                                                            APPLICANT: MAIC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: ABRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID MOS: 33142
SEC IT NO 11000
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Best Local
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Best Local Similarity
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TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 107
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    J. Rubenfield et al.
    ION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
    ION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
    107196.136

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100.0%; Pred. No.
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100.0%; Pred. No. 75
ive 0; Mismatches
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75;
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; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-8104
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US-09-107-532A-3059
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Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm
TITLE OF INVENTION: NUCLEIC ACID
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Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
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Matches 17; Conserval
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LENGTH: 1134
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Best Local
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 66/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
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                                              APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                        ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
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17; Conserv
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                                                                                                                                                                                                                    COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                               CITY: Waltham
STATE: Massachusetts
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
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Pred. No.
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AND AMINO ACID SEQUENCES RELATING TO
FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
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75;
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75;
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GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CCURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,786

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...1281
SEQUENCE DESCRIPTION: SEQ ID NO: 3059:
US-09-107-532A-3059
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US-09-252-991A-12508
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                                                                                                                                                         RESULT 34
US-09-023-655-293/c
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Best Local Similarity
The 17; Conserva
                                                                                                                                                                                                                                                                                                                                                                              US-09-252-991A-12508
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SEQ ID NO 12508
LENGTH: 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 12508, Application US/09252991A Patent No. 6551795
                                                                                                                         Sequence 293, Application US/09023655 Patent No. 6607879
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Best Local Similarity
                                                                                                        GENERAL INFORMATION:
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TELEPHONE: (781)893-5007
TELEPAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 3059:
                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
               APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1281 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                   1079 TGCCGTCCAGCCGGCGC 1095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            766 GGAGAACATCATGTTGC 782
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                                                                                                                                                                                                                                                                                                    ilarity 100.0%;
Conservative (
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100.0%; Pred. No.
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                                     FOR
                                    THE DETECTION OF BLOOD CELL
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INCYTE PHARMACEUTICALS, INC

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US-09-252-991A-8001
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                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8001
LENGTH: 171.
                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION: APPLICANT: Marc J.
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Matches 17; Conserv
                                                       Matches
                                                                                       Query Match
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                                                                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (650) 845-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                       LENGTH: 1314
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS: 1
TOPOLOGY: line
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                    y Match 1.6%; Score 17; DB 4; Local Similarity 100.0%; Pred. No. 76; nes 17; Conservative 0; Mismatches
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CITY: 1
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291 CGGCCAGTTCGCCATCG 307
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CALIFORNIA
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                                                                                                                                                                                                                                                                                                                                                   Marc J. Rubenfield et al.
VENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
VENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3174 PORTER DRIVE
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845-4166
MO: 293:
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                                                                                       Length 1314;
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PILE REFERENCE: 794CIP2B
CURRENT APPLICATION UNIMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
SEQ ID NO 1058
LENGTH: 1450
TYPE: DNA
GRANNEW
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-2821
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US-09-252-991A-2821/c
; Sequence 2821, Application US/09252991A
; Patent No. 6551795
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US-09-620-312D-1058
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APPLICANT: Marc J. Rubenfield et al.

APPLICANT: MARC J. Rubenfield et al.

APPLICANT: MICLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEG ID NOS: 33142

SEQ ID NO 2821

LENGTH: 1431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6569662 GENERAL INFORMATION:
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APPLICANT:
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                                                                                                                                                                                                                                                                         APPLICANT: Drmanac, Radoje T.
IITLE OF INVENTION: No. 6569662el Nucleic Acids
IITLE OF INVENTION: Polypeptides
ORGANISM: Homo sapiens FEATURE: NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                            PPLICANT:
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Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
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Xue, Aidong J.
Yang, Yonghong
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Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Jian-Rui
Zhou, Ping
                                                                                                                                                                                                                                                                                                                                                                                             Ma, Yunging
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di, Vinod
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100.0%; Pred. No.
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CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8133
LENGTH: 1755
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PATENTIN Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1815
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic B.t. to
US-09-178-252-3
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US-09-178-252-3
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APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3-09-252-991A-8133/c
Sequence 8133, Application US/09252991A
Patent No. 6551795
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/09178252
Patent No. 6218188
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Best Local
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                                                                                                                                                                                   APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.
APPLICANT: Marva, Kenneth E.
APPLICANT: Marva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2
CURRENT APPLICATION NUMBER: US/09/178,252
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER TILING DATE: 1998-03-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1755
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: (1)...(1450)
OTHER INFORMATION: n = a,t,c
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17; Conserv
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; Pred. No. 76; 
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/178,252
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Synthetic B.t. toxin gene US-09-178-252-7
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                                                                            ; OTHER INFORMATION: Synthetic B.t. toxin gene US-09-178-252-8
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Best Local S
Matches 17
                                                                                                                                                                                    TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal FILE REFERENCE: MA.714XC2
CURRENT APPLICATION NUMBER: US/09/178,252
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 60/065,215
EARLIER FILING DATE: 1997-11-12
EARLIER FILING DATE: 1997-11-12
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER APPLICATION NUMBER: 60/076,445
EARLIER FILING DATE: 1998-03-02
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PATENTIN Ver. 2.0
SOFTWARE: PATENTIN Ver. 2.0
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Best Local S
Matches 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09178252 Patent No. 6218188
Query Match 1.6%; Score 17; Best Local Similarity 100.0%; Pred. No. Matches 17; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cardineau, Guy A. APPLICANT: Stelman, Steven J. APPLICANT: Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Cardineau, Guy A. APPLICANT: Stelman, Steven J. APPLICANT: Narva, Kenneth E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins FILE REFERENCE: MA-714XC2
                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1815
TYPE: DNA
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                                                                                                                    FEATURE:
                                                                                                                                                                          LENGTH: 1815
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17; Conserv
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100.0%; Pred. No.
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                    DB
76;
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Mismatches

Indels

0

Gaps

CTGCCTCAACAATCCTG

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Sequence 7, Application US/09826660

Patent No. 6673990

Patent No. 6673990

Patent No. 6673990

APPLICANT: Cardineau, Guy A.
APPLICANT: Stelman, Steven J.

APPLICANT: Stelman, Steven J.

PILE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins FILE REFERENCE: MA-714XC2D1

CURRENT APPLICATION NUMBER: US/09/826,660

CURRENT APPLICATION NUMBER: 09/178,252

PRIOR APPLICATION NUMBER: 00/65,215

PRIOR APPLICATION NUMBER: 60/65,215

PRIOR APPLICATION NUMBER: 60/65,215

PRIOR APPLICATION NUMBER: 60/076,445

PRIOR FILING DATE: 1997-11-12

PRIOR FILING DATE: 1998-03-02

NUMBER OF SEQ ID NOS: 27

SOFTMARE: Patentin Ver. 2.0
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                                                                 ; OTHER INFORMATION: Synthetic B.t. toxin gene US-09-826-660-7
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US-09-826-660-3
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US-09-826-660-7
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LENGTH: 1815
TYPE: DNA
ORGANISM: Artificial Sequence
Query Match
Best Local Similarity
                                                                                                                                                                                                 SEQ ID NO 7
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APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth E.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714XC2D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/076,445 PRIOR FILING DATE: 1998-03-02 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/826,660 CURRENT FILING DATE: 2001-04-05 PRIOR APPLICATION NUMBER: 09/178,252 PRIOR FILING DATE: 1998-10-23 PRIOR APPLICATION NUMBER: 60/065,215 PRIOR FILING DATE: 1997-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE: OTHER INFORMATION: Synthetic B.t. toxin gene
                                                                                                          FEATURE:
                                                                                                                                                                      ENGTH: 1815
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  1.6%;
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100.0%; Pred. No.
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    Score 17;
Pred. No.
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    DB 4;
76;
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APPLICANT: Hu, Ping
APPLICANT: Rutter, Marc
APPLICANT: Wang, Jian-Wang
APPLICANT: Wang, Jian-Wang
TITLE OF INVENTION: No. 6399761el Human Potassium Channels
FILE REFERENCE: SEQ-15P
CURRENT APPLICATION UNMEER: US/09/336,643A
CURRENT FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 60/076.687
PRIOR TILING DATE: 1998-08-07
PRIOR TILING DATE: 1998-08-07
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: 60/116,448
PRIOR APPLICATION NUMBER: DCT/US99/03826
PRIOR FILING DATE: 1999-01-19
PRIOR FILING DATE: 1999-02-22
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US-09-826-660-8
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                                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 11
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SEQ ID NO 8
LENGTH: 1815
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Miller, Andrew P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/09336643A Patent No. 6399761
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Best Local Similarity
Matches 17; Conserv
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Patent No. 6673990
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APPLICANT: Stelman, Steven J.
APPLICANT: Stelman, Steven J.
APPLICANT: Narva, Kenneth B.
TITLE OF INVENTION: Plant-Optimized Genes Encoding Pesticidal Toxins
FILE REFERENCE: MA-714KC2D1
CURRENT APPLICATION NUMBER: US/09/826,660
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: 09/178,252
PRIOR APPLICATION NUMBER: 09/076,445
PRIOR APPLICATION NUMBER: 60/076,445
PRIOR PILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
PRIOR FILING DATE: 1998-03-02
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ORGANISM: Artificial Sequence
FEATURE: NAME/KEY: CDS
LOCATION: (383)...(1157)
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                                                             ORGANISM: H. sapiens
                                                                                                    ENGTH: 1862
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76;
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Search completed: June 30, 2004, 21:26:53 Job time : 100 secs В ; OTHER INFORMATION: K+Hnov15 US-09-336-643A-11 Query Match 1.6%; Score 17; DB 4; Length 1862; Best Local Similarity 100.0%; Pred. No. 76; Matches 17; Conservative 0; Mismatches 0; Indels 673 ACAAGCATGCAGCCAGC 689 0; Indels 0; Gaps 0;

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-Q=/cgn2 | 1/USFTO spcol/cBBREYESUS641/runat_29062004_143151_24567/app_query.fasta_1.519
-DB=EST -QFWT=fastap_SUFFIX=rst -MINMARCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TPANUS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE-pct -THR MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-DUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINILEN=0 -MAXIEN=200000000
-USER-GEBREYESUS641_@CNN 1 1 2810 @runat 29062004 143151_24567 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WANIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -THREADS=1 -XGAPEP=10 -XGAPEXT=0.5 -FGAPOP=6
-PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Ygapop 10.0
Fgapop 6.0
Delop 6.0
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Copyright (c) 1993 - 2004 Compugen Ltd.
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em_htc:*
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(without alignments)
3398.565 Million cell updates/sec
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## 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

45	44	43	42	41	40	6. C	ა მ	37	<b>3</b> 6	ω U	υ 4	ယ	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	110	1,0	ь (	00 -	J 0	ית	ָח ת	۱ م	ادر	N I		Result No.
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6 6024497	782 60307492	B741392 AMGNNUC:	17803 mh47a03.r	929308 UI-E-	F547702 UI-R-A0-	279	Q071749 AGENCOUR	42106	Q069289 AC	E306065 6011017	476323 uq73f11.	3365 6015679	742180 up53c09.	212667 mw78f	588 60175853	F727181 by	071271 AGEN	419640 60	F019568 ux12f1	1414743 60299113	38 60316865	I652999 60329997	1690902 60331204	G968192 60283567	E848999 uw01g07	A529114 8094-35	.763351 vw53c11	F162798 601769	C023238 Mus musc	G865492 60278362	G277312 ux42b	12103 ux53g	Q945722 AGENCOUR	G968191 602	A334157 NISC	I149425 602	C012210 Mus	1554559 603	F617168 AGE	F617929 AGENCOUR	U513845 AGENCOUR	U671103 NISC 1r0	841154 AGENCOUR	0814 NI	9

## ALIGNMENTS

RESULT 1
BU670814
BU670814
BU670814
BU670814
BU670814
INCI 101e11.y1 NCI CGAP Pr49 Rattus norvegicus cDNA clone
IMACE:5598044 5', mRNA sequence.
BU670814
VERSION
BU670814
VERSION
EST.
SOURCE
SOURCE
ORGANISM
Rattus norvegicus (Norway rat)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

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JOURNAL COMMENT
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Query Match:
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cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consorti
DNA Sequencing by: National Institutes of Health
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1997)
Contact: Robert Strausberg, I
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 666)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: LLAM12384
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LeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPheGluAsnLysThr
                                                                                         CGCCTGCCGTCCAGCCGGCGCGTGTGAGCCGTGAGGAGATCGAGCGCGAGGTGAGCATC
                                                                                                                      ArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArgGluValSerIle
                                                                                                                                                                                               CGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGCGGCCAAGTTCATAAAGAAGCGG
                                                                                                                                                                                                                                       ArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPheIleLysLysArg
                                                                                                                                                                                                                                                                                                                                                              ProSerSerGlySerAlaAlaLeuSerCysSerPheProHisSerGlyPheAlaIleVal 102
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                                                                                                                                                                                                                                                                                                                -GGCAGCGGCCAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev stage="adult, 11 week"
/lab_nost="DH10B (T1 phage-resistant)"
/lab_nost="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Pr49"
/note="forgan: prostate; Vector: pCMV-SPORT6.1; Site_1:
/note; Site_2: EcoRV; Cloned unidirectionally. Primer:
Oligo dT. Pool of 3 primary libraries: NCI_CGAP_Pr30
(ventral prostate from 11 wk male, 3 days
post-castration, average insert size 2 kb), NCI_CGAP_Pr40
(ventral prostate from 11 wk male, 5 days
post-castration, average insert size 1.6 kb) and
NCI_CGAP_Pr41 (ventral prostate from 11 wk male, 7 days
post-castration, average insert size 2.5 kb). Constructed
by Life Technologies/Invitrogen. Note: this is a NCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_CGAP_INCI_C
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post-castration"
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db_xref="taxon:10116"
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80.37%
76.17%
40.42%
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REFERENCE
AUTHORS
TITLE
                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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BU841154
LOCUS
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SOURCE
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FIGURE9 (1-361) x BU841154
                                                                                                                                                        Alignment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BU841154 947 bp
AGENCOURT 10187633 NIH_MGC_134 Mus
IMAGE:6518980 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 947)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                         /tissue type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_134"
/note="Vector: pCMV-SPORT6.1; Site_1: EcoRV; Site_2: Not1;
Cloned_unidirectionally. Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NIH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6518980"
                                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
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RESULT 3
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                                                                                                                Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                    BU671103 597 bp mRNA linear I
NISC lr05b04.y1 NCI CGAP Pr49 Rattus norvegicus cDNA
IMAGE:5598270 5', mRNA sequence.
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                           BU671103.1 GI:23399332
                                             Tumor Gene Index
                                                         NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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 {\tt laSerArgThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGln}
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Best Local Similarity:
Query Match:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
cDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
info@image.llnl.gov
Plate: LLAM12385 row: C column: 7
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Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
                                                                                                          erTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgA
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rgThrSerCysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuA
                                                                                                                                                                                  TTTCTGGCTGAGAAGGAGTCACTGACAGAGGATGAGGCCACGCAGTTCCTCAAGNCAGAT
                                                                                                                                                                                                                                                                                                GAGAACAAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGCGAACTTTTCGAC
                                                                                                                                                                                                                                                                                                                                               GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGGGGGTGTGAGCCGTGAGGAGATCGAGCGC
                                                                       CCTGGACGGTGTCCACTACCTGCACTCCAAGCGCATCGCGCACTTTGACCTGAAGCCGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev stage="adult, 11 week"
//lab_host="DH10B (T1 phage-resistant)"
//lab_host="DH10B (T1 phage-resistant)"
//clone_lib="NCI_CGAP_pr49"
//clone_lib="NCI_CGAP_pr49"
//clone_Torgan: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Corgan: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Corgan: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Corgan: prostate from 11 lbraries: NCI_CGAP_pr30
//entral prostate from 11 wk male, 3 days
post-castration, average insert size 2 kb), NCI_CGAP_Pr40
//entral prostate from 11 wk male, 5 days
post-castration, average insert size 1.6 kb) and
NCI_CGAP_pr41 (ventral prostate from 11 wk male, 7 days
post-castration, average insert size 2.5 kb). Constructed
by life Technologies/Invitrogen. Note: this is a NCI_CGAP_pr41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="ventral prostate,
post-castration"
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/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="male"
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725.00
95.62%
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39.70%
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RESULT 4
BU513845
LOCUS
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Best Local Similarity:
Query Match:
DB:
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AUTHORS
TITLE
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No..
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA Library Preparation: Invitrogen Corp
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Muri
1 (bases 1 to 971)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
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BU513845.1 GI:22821371
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AGENCOURT 10110388 NIH MGC 134 Mus

IMAGE: 6510429 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. David Rowe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
PheLeuAlaGluLysAsp-His***GlnArgMetArgProArgSerSerSerSerSerArgSe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATCGCGCACAGGATCGAGGCCGGTAGCGAGGTTCAAGAACATCTTTGGCACGCCAG
                                                                               GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp
                                                                                                                   GAGGTGAGCATCCTGCGCGAGATCCGCCAACCCCAACATCATAACACTGCATGACGTGTTC
                                                                                                                                                GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
                                                                                                                                                                                 ATCAAGAAGCGGCGCCTGCCATCCAGCCGGCGGTGTGAGCCGGGAGGAGCATCGAACGC
                                                                                                                                                                                                    IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg
                                                                                                                                                                                                                                                                  PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe
                                                                                                                                                                                                                                                 TTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="undifferentiated limb"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH_MGC_134"
/note="Vector: pcMV-SPORT6.1; Site_1: EcoRV; Site_2: NotI;
Cloned_unidirectionally_Primer: Oligo dT. Average insert
size 1.7 kb. Constructed by ResGen, Invitrogen Corp. Note:
this is a NHH_MGC_Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:6510429"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Mus musculus"
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725.00
77.31%
77.31%
73.61%
39.70%
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Matches:
Conservative:
Mismatches:
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Gaps:
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AUTHORS
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SOURCE
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CF617929
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National Institutes of Health, Mammalian
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
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CF617929.1 GI:37235384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (bases 1 to 844)
                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                            organism="Mus musculus"
```

```
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Naryan Bhat
CDNA Library Preparation: Express Genomics
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDAM607 row b column: 03
High quality sequence stop: 668.
Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pLeuGlySer***TyrValGluHisArgArgHisHisLeuHisPro 311
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/clone_lib="NIH_MGC_222"
/note="Organ: placenta; Vector: pExpress-1; Site 1: EcoRV;
Site 2: Not1; RNA obtained from three placentas from
female C57/BL6 mouse at 16 days pregnancy. Tissues were
snap-frozen and kept at -80C for two days before RNA
extraction and purification (Tri-reagent method). cDNA was
primed using oligo-dT primer:
5'-pGACTAGTTCTAGATCGCGACCGCCCC(T)25-3' and cloned into
the EcoRV/NotI sites of pExpress-1. Size-selection >1 kb
resulted in an average insert size of 1.5 kb. Library is
                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:30525626"
/lab_host="DH10B_(phage-resistant)"
/clone_lib="NIH_MGC_222"
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Query Match: DB:

FIGURE9

(1-361) x CF617929 (1-844)

Percent Similarity: Best Local Similarity:

6e-40 722.00 73.82% 69.96% 39.54%

Alignment

No.:

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146 TTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTC
                                                               850 bp
AGENCOURT 15774334 NIH MGC 204 Mus
IMAGE:30526684 5', mRNA sequence.
CF617168
CF617168.1 GI:37234028
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Tissue Procurement: Naryan Bhat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
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Contact: Daniela S. Gerhard,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Office of Cancer Genomics
                                                                                                                                                                                    GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp
                                                                                                                                                                                                                                                                            GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
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                                                                                                                                                                                                                                                                                                                                         ATCAAGAAGCGGCGCCTGCCATCCAGCCGGCGCGGTGTGAGCCCGGGAGGAGATCGAACGC
rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgAr
                                                     PheLeuAlaGluLysAsp-His***GlnArgMetArgProArgSerSerSerSerArgSe
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/clone lib="NIH MGC 204"
/clone lib="NIH MGC 204"
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/incte="Organ: placenta; Vector: pExpress-1; Site 1: EccRV;
/incte="Organ: placenta; Vector: pExpress-1; Site 1: EccRV;
/incte="Organ: placenta; Vector: pExpress-1; Site 2: McC II; Site 3 from female C57/BL6 mouse at 16 days perganator. Tissues were snap-frozen and kept at -80° for two days before RNA extraction and purification (Tri-reagent method). cDNA was primed using oligo-dT primer:
// permethod of primer:
// permethod of primer:
// permethod of permethod of pExpress-1. Size-selection >0.75kb
// resulted in an average insert size of 1.1 kb. This
// primery, nanoquantity library is normalized to Cots
// (non-normalized primary) library is NIH MGC 223) and was
// constructed by Express Genomics (Frederick, MD)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
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/clone="IMAGE:30526684"
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KEYWORDS SOURCE ORGANISM ACCESSION VERSION

Mus musculus

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High qualcores:	Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Crania Eukaryota; Metazoa; Chordata; Sciuro 1 (bases 1 to 972) NH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mamma Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green cDNA Library Preparation: Life Tech cDNA Library Preparation: Life Tech cDNA Library Arrayed by: The I.M.A. DNA Sequencing by: Incyte Genomics, Clone distribution: MGC clone distr found through the I.M.A.G.E. Consort http://image.lnil.gov Plate: LiAM11785 row: i column: 23	296 rpLeuGlySer***TyrValGluHisArgArgHis 668 GGCTTGGAGGCTGACARGTGGAGCATTGGCGTCAT 316 spGlyGlnGlyProGlnThrValProAlaArgGly 721	455 CTAGACGGTGTCCACTACCTGCACTCCAAG 216 GThrSerCysCysTrpThrSerMetGlnPr 216 GThrSerCysCysTrpThrSerMetGlnPr 216 AACATCATGTTGCTGGACAAGCACGCAGCC 236 ASerArgThrGlySerArgProValAlase 216 ACATCATGTTGCTGGACAAGCACGCAGGCAGCACGCACGC
Lity sequence stop: 845. Location/Qualifiers  1. 972 (roganism="Mus musculus" /roganism="Mus musculus" /mol type="mRNA" /strain="ryb/N" /clone="IMAGE:5310046" /clone="IMAGE:5310046" /clone="IDH10B (T1 phage-resistant)" /clone="IDH10B (T1 phage-resistant)" /clone="IDH10B (T2 phage-resistant)" /clone="IDH10B (T3 phage-resistant)" /clone="IDH10B	Mus musculus (house mouse) Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Mus. 1 (bases 1 to 972) 1 (bases 1 to 972) NIH-MSC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. cDNA Library Preparation: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11785 row: i column: 23	pLeuGlySer***TyrValGluHisArgArgHisHisLeuHisProValSerAla***A 316	CTAGACGGTGTCCACTACCTGCACTCCAAGCCCATCGCACACTTTGACCTGAAGCCCGAG 514  GThrSerCysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuAl 236  [
RESULT 8 BC012210 LOCUS BC012210 Mus musculus death-associated kinase 3, mRNA linear HTC 19-NOV-2003 DEFINITION Mus musculus death-associated kinase 3, mRNA (cDNA clone IMAGE:3993055), with apparent retained intron.  ACCESSION ACCESSION BC012210.1 GI:15126556 KEYWORDS Mus musculus (house mouse) Mus musculus (house mouse) Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.  1 (bases 1 to 976) Klausner, R.D., Collins, F.S., Wagner, L., Shennen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Babat, N.K., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,	5 2 5 4 2 7 5 3 1 5 3 1 7 9 4 7 6 3 1 7 9 4 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7 8 7	107 245 177 305 196 216 216	st Local Similarity: 69.96% Mismatches: 21 ery Match: 12 39.54% Indels: 40  ;  Gaps: 5  gure9 (1-361) x BI554559 (1-972)  99    pheAlaIleValArgLysCysLysGlyThrGlyMetGluTyrAlaAlaLysPhe

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Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., J., Lu,X., Gibbs,R.A.,
Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
LPTOC. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                (1-361) x BC012210 (1-976)
    164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-AUG-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: Lothar Hennighausen Ph.D., Robin Hump
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
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Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, ;
Kowis, C.R., Sneed, A.J., Martin, R.G., Muzny,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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Contact: MGC help desk
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  TTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTC
                          PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe
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Conservative:
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                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Rodentia; Sciurognath
1 (bases 1 to 681)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            602848986F1 NCI_CGAP_Lu29
                                  found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11063 row: 1 column: 22
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Mus musculus (house mouse)
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Location/Qualifiers
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637 bp mRNA linear EST 04-NOV-2002
NISC_1s06b10.y1 NCI_CGAP_Pr50 Rattus norvegicus cDNA clone
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/lab host="DH10B"
/clone_lib="NCI_CGAP_Lu29"
/note="Organ: lung: Vector: pCMV-SPORT6; Site_1: Sall; Site_2: NotI; Cloned unidirectionally. Primer: Oligo cibrary constructed by Life Technologies. Investigator providing samples: Gilbert Smith, NIH"
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/mol_type="mRNA"
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strain="Czech II"
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ORGANISM
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

DNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)

Clone distribution: NCI-CGAP clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:

info@image.llnl.gov

Plate: LLAM12388 row: C column: 20
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Rattus norvegicus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMAGE:5599435 5', mRNA sequence.
CA334157
CA334157.1 GI:24552255
EST.
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Contact: Robert Strausberg,
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
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GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp
                                                                                GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
                                                                                                                                                       | IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg
                                                                                                                                                                                                                                         PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe 116
                                                                                                                            ATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGCGCGTGTGAGCCGTGAGGAGATCGAGCGC
                                                                                                                                                                                                               TTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGCGGCCAAGTTC
                                            GAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCATCACGCTGCACGATGTGTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 te: LLAM12388 row: C column: primer: M13RP1 reverse primer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="dult, 11 week"

//Ab host="DHJOB (T] phage-resistant)"

//Clone lib="NCI_GAP_PT50"

//Clone lib="NCI_GAP_ET50"

//Clone lib="NCI_GAP_ET50"

//Note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
//NotI; Site_2: EcoRV; Cloned unidirectionally. Primer:
Oligo dT. Pool of 3 primary libraries: NCI_GAP_PT39

(dorsolateral prostate from 11 wk male, 3 days
post-castration, average insert size 2.7 kb),
NCI_GAP_PT29 (dorsolateral prostate from 11 wk male, 5
days post-castration, average insert size 2.2 kb) and
NCI_GGAP_PT42 (dorsolateral prostate from 1 wk male, 7
days post-castration, average insert size 2.2 kb).

Constructed by Life Technologies/Invitrogen. Note: this is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="dorsolateral prostate,
7-days post-castration"
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/sex="male"
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/db_xref="taxon:10116"
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                                                              FIGURE9 (1-361) x BG968191 (1-887)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                           No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11005 row: c column: 20
High quality sequence stop: 820.
Location/Qualifiers
1. 887
Location/Qualifiers
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99 PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe 116
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 887)
1 (bases 1 to 7/22 noi nih nov/)
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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EST.
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602835674F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4990027 5',
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/db_xref="taxon:10090"
/clone="IMAGE:4990027"
/lab host="UH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site 1: NotI;
/note="Organ: colond unidirectionally. Primer: Oligo dT.
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
                                                                                                      5.56e-39
708.50
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Mismatches:
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RESULT 12 BQ245722 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	B 6	da da	עס	dd Qy	QQ dQ	QQ VQ	90 Qy	Db Db	Db Db	da Qy	ДУ	Db
BQ945722  BQ945722  BQ945722  ON AGENCOURT 8953288 NCI CGAP CO24 Mus musculus cDNA clone IMAGE:6477473 5', mRNĀ sequence.  BQ945722  NO BQ945722  Mus musculus (house mouse)  SM Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  E 1 (bases 1 to 936)  E 1 (bases 1 to 936)  S NIH-MGC http://mgc.nci.nih.gov/.  National Institutes of Health, Mammalian Gene Collection (MGC)  Unpublished (1999)  Contact: Robert Strausberg, Ph.D.  Email: ggapbs-r@mail.nih.gov  Tissue Procurement: The Cepto Laboratory  CDNA Library Preparation: Life Technologies, Inc.  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  DNA Sequencing by: Agencourt Bioscience Corporation  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  Plate: LLAM14019 row: h column: 18  High quality sequence stop: 708.	316 spGlyGlnGlyPro 320	96 rpleuGlySer***Tyr          77 GGCTTGGAGGCTGACAT	276 euThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrThrT 296	256 rSerValArgGlyArgCysGlyHisHisPro-IleGly***IleLeuHisGlyLeuGlyL 276	236 aSerArgThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGlnSerSe 256	216 gThrSerCysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuAl 236	196 rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgAr 216	177 PheLeuAlaGluLysAsp-His***GlnArgMetArgProArgSerSerSerSerSerArgSe 196	157 GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp 176 	137 GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe 156 	117 IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg 136	164 TTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTC 223

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                                                                                                                                             euThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrThrT
                                                                                                                                                                                                        erSerValArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyL 276
                                                                                                                                                                                                                                                                                              AACATCATGTTGCTGGACAAGCACGCAGCCAGCCCCCGCATTAAGCTCATCGACTTTGGC
                                                                                                                                                                                                                                                                                                                                                        CTAGACGGTGTCCACTACCTGCACTCCAAGCGCATCGCACACTTTGACCTGAAGCCCGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCATAACACTGCATGACGTGTTC
                             spGlyGlnGlyProGlnThrValProAlaArgGlyProGlyIleArgAlaGly-----
                                                           GGCTTGGAGGCTGACATGTGGAGCATTGGCGTCATCACCTACATCCTCCTGAG---
                                                                                rpLeuGlySer***TyrValGluHisArgArgHisHisLeuHisProValSerAla***A
                                                                                                                                                                                                                                        ATCGCGCACAGGNATCGAGGCTGGCAGCGAGTTCAAGAACATCTTTGGCA------
                                                                                                                                                                                                                                                                                                                                                                               rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgAr
                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="IMAGE:6477473"
/lab host="PHIOB (T1 phage-resistant)"
/clone_lib="NGI_CGAP_Co24"
/note="Organ: colon, Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo d'Average insert size 1.6 kb. Constructed by Life Average insert size 1.6 kb. Constructed by Life
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Mus musculus"
/mol_type="mRNA"
/strain="FVB/N"
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61.09%
38.31%
   CGGAGCGTCCCCATTCCTGGGCGAGAC---CAAGCAGGAGACGCTG
                                                                                                                    CACCCGAG-TTTGTCGCCCCCGAGATCGTGAACTATGAGCCACTTT
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RESULT 13
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Verte
Mammalia; Eutheria; Rodentia; Sciurognathi; M
1 (bases 1 to 696)
NCI-GGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
Tumor Gene Index
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BF012103
BF012103.1 GI:10712378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1997)
Other_ESTs: ux53g01.x1
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GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
                                                    | IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg
                                                                                           TTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTC
                                                                                                                   PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe 116
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                               ATCAAGAAGCGGCGCCTGCCATCCAGCCGGCGCGCGGGTGAGCCGGGAGGAGCATCGAACGC
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/db_xref="taxon:10090"
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Eutheria; Rodentia;
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699.00
72.53%
68.67%
38.28%
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Matches:
Conservative:
Mismatches:
Indels:
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                   UX42D06.Yl Soares NMMAX maxillary process Mus muscullus cDNA clone IMAGE:3512794 5' similar to TR:054784 O54784 DEATH-ASSOCIATED KINASE 3', mRNA sequence.

BG277312
BG277312.1 GI:13072489
                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
Other_ESTs: ux42b06.x1
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 710)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                           Mus musculus
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                                                                                                             quality sequence stop: 477.
Location/Qualifiers
/organism="Mus musculus"
/mol type="mann,"
/db_xref="taxon:10090"
/clone="IMAGE:3512794"
/tissue_type="maxillary process"
/lab_host="DH10B (phage-resistant)"
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 mRNA sequence.
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BG865492.1 GI:
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В ΛÕ 멍 Ş В δ

> the Not CDNA 3′],

Percent Similarity:
Best Local Similarity:
Query Match:
DB: (1-361) x BG277312 (1-710) 296 632 276 622 256 573 236 513 216 453 196 393 177 S S S 157 273 137 213 117 153 99 BG865492 602783624F1 aSerArgThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGlnSerSe gThrSerCysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuAl GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg GGCTTGGAAGCTGACATGTGGAGCATTGGCGGCATCACCTACAT rpLeuGlySer\*\*\*TyrValGluHisArgArgHisHisLeuHis 310 ATCGCGCACATGATCGAGGCTGGCAGCGAGTTCAAGAACATCTTTTGCA-----ATCATCATGTTGCTGGACAAGCACGCAGCCAGCCTCCGCATTAAGCTCATCGACTATGAC rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr\*\*\*SerArgAr PheLeuAlaGluLysAsp-His\*\*\*GlnArgMetArgProArgSerSerSerSerArgSe GAGAACAAGACAGATGTGGTGCTGATCCTGGAGCTGGTGTCCGGTGGCGAGCTTTTCGAC GAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCATAACACTGCATGACGTGTTC TTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGAGTATGCAGCCAAGTTC PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe 116 euThrCysLeuAsnAsnProValPheHisSerPro\*\*\*AspCysLysLeu\*\*\*ThrThrT rSerValArgGlyArgCysGlyHisHisPro-IleGly\*\*\*IleLeuHisGlyLeuGlyL CTAGACGGTGTCCACTACCTGCACTCCAAGCGCATCGCACACTTTGACCTGAAGCCCGAG ATCAAGAAGCGGCGCCTGCCATCCAGCCGGCGGGTGTGAGCCGGGAGGAGATCGAACGC NCH 3.14e-38 695.50 75.93% 71.76% 38.09% -----CACCCGAGTT-----SG2 703 Mus Conservative: Mismatches: Indels: Gaps: Length: Matches: musculus CGTCCCCGAGATCGAGAACTATGAGCCACTT mRNA CDNA 710 955 19 33 linear EST 29-MAY-2001 clone IMAGE:4910045 5', 296 156 631 276 572 236 452 196 176 136 212 621 216 392 332 272

Db 353 TTCCTGGCCGAGAAGGAATTGACGAGATGAAGCCAGCCAG	233 GAGGTGAGCATCCTGCGCGAGATCCGCCCAACATCATAACACTGCATGACGTGTTC 29 157 GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp 17	PIGURE9 (1-361) x BG865492 (1-703)  Qy  9 PheAlaIleValArgLysCysLysGlyThrGlyMetGluTyrAlaAlaLysPhe 116	Alignment Scores: 7.43e-38 Length: 703 Pred. No.: 690.00 Matches: 161 Score: 690.00 Matches: 161 Percent Similarity: 74.78\$ Conservative: 8 Best Local Similarity: 71.24\$ Mismatches: 21 Query Match: 37.79\$ Indels: 37 DB: 6aps: 5	FEATURES  Location/Qualifiers  1. 703  1. 703  1. 703  1. 703  2. 703  // 103  // 203	KEYWORDS  SOURCE  Mus musculus (house mouse)  ORGANISM Mus musculus  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  1 (bases 1 to 703)  AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.  TITLE  National Institutes of Health, Mammalian Gene Collection (MGC)  JOURNAL  Contact: Robert Strausberg, Ph.D.  Email: cgapbs-r@mail.nih.gov  Tissue Procurement: Jeffrey E. Green, M.D.  cDNA Library Preparation: Life Technologies, Inc.  cDNA Library Preparation: Life Technologies, Inc.  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  http://image.llnl.gov  Plate: LLAM10809 row: o column: 06  High forality sequence stop: 701.
				Search completed: June 30, 2004, 22:20:02 Job time : 3179 secs	Qy       236       aSerArgThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGlnSerSe       256         Db       533       ATCGCCACAGGATCGAGGCTGGCAGCGAGTTCAAGAACATCTTTGGCA

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## ALIGNMENTS

Rat myosin phosphatase targeting subunit 1-kinase, MYPT1 kinase, cDNA.

28-NOV-2002 ABS54622;

(first entry)

ABS54622 standard; cDNA; 1093 BP.

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Best Local Similarity
Matches 1093; Conserv
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P-PSDB;
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                                                                              Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
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15-MAR-2002; 2002US-0364045EP
15-MAR-2002; 2002US-0364055EP
30-DEC-2002; 2002US-0436643EP
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toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
                                                      Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3594.
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                                                                             The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                Mendrick
Elashoff
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                                                                                                                                                                                                                                                                                                                                         Determining if a compound induces a toxic effect on a tissue or cell, identifying hepatotoxic compounds, comprises comparing a gene express; profile of a tissue or cell sample to a database of Tox mean and non-
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                                                        Sequence 1514
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04-SEP-2002;
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The present invention describes oligonucleotide libraries for detecting messenger RNAs that populate a (sub-)transcriptome, where the (sub-)transcriptome comprises messenger RNAs transcribed from multiple transcription units that populate a genome. The library comprises several oligonucleotides, each capable of hybridising selectively to a set of messenger RNAs transcribed from a given transcription unit of the genome, which encodes one or more messenger RNA splice variants. The
                                                                                                                                                                                                                                                                                          New oligonuclectide libraries comprising oligonuclectides which selectively hybridize to mRNAs transcribed from a transcription unit of genome, useful for detecting tissue-, pathology-, and developmental-
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02-MAY-2001;
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                                                                                                                                                                                                               SEQ ID NO 3053; 47pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wasserman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0221607P.
2001US-0287724P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mintz
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                                                                                                                                                                                                                                                                                                                                                                                                                                               М
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mintz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Faigler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA transcript;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NO:3053
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Best Local S
Matches 44
                                       The invention provides human and murine recombinant Zipper Interpretein Kinase (ZIP-kinase) proteins. These proteins are sering kinases which bind the leucine zipper domain of transcription of ATF4. Host cells containing vectors comprising the ZIP-kinase acids are used for the recombinant expression of the proteins. protein and DNA are useful as gene therapeutic agents against o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and pathology-specific genes such as those genes only expressed in specific tissue under a specific pathological condition; to detect developmental specific genes; and to detect RNA transcripts and splice variants of a transcriptome of a patient suffering from a particular disorder. ABN27253 to ABN59589 represent oligonucleotide sequences from rats, humans and mice, which are used in the exemplification of the present invention. N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quantitatively characterising the corresponding transcriptome, and detecting RNA transcripts and splice variants of human or animal transcriptomes. The libraries may also be used as specialised minilibraries to detect transcripts of a sub-transcriptome under a par biological or pathological state, and so allowing the detection of
                                                                                                                                                                           New
and
                                                                                                                                                                                                                                                                                                                                                                                                                  EP911408-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oligonucleotide libraries are useful for detecting mRNAs from biological sample, in expression profiling studies, in qualita
                                                                                                                                               Claim 6;
                                                                                                                                                                                                                                                                                                                           26-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                         24-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; murine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Murine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX34657 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 65
                         as anti-cancer agents. The present sequence
                                                                                                                                                                                                                        P-PSDB;
                                                                                                                                                                                                                                                                 Akira S,
                                                                                                                                                                                                                                                                                                                                                                                       28-APR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zipper Interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAX34657;
                                                                                                                                                                                                                                                                                             (NISC-) JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         leucine zipper
                                                                                                                                                                          DNA,
                                                                                                                                                                                          Recombinant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CACAGGATCGAGGCGGGTAGCGAGTTCAAGAACATCTTTGGCAC 44
            kinase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP; 16 A; 19 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                               19-22;
                                                                                                                                                                                                                                                                                             SCI &
                                                                                                                                                                                                                                                                                                                           97JP-00261589
                                                                                                                                                                                                                                                                                                                                                         98EP-00307747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain; transcription factor ATF4; gene therapy;
                                                                                                                                                                           Zipper Interacting as anticancer agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (serine/threonine
                                                                                                                                                                           anticancer agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein Kinase; ZIP-kinase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA; 1429
                                                                                                                                                                                                                                                                                               TECHNOLOGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%;
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Pred. No
                                                                                                                                                                                                                                                                                               CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               red. No. 1.:
Mismatches
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                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       kinase)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.2e-1:
                                                                                                                                                                                           Kinase (ZIP-kinase)
                            represents a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          serine/threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in qualitatively on scriptome, and in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA.
                                          against cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     electronic format
                          DNA encoding
                                                                                                   serine/threonine
                                                                                                                    Interacting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a particular
                         ZIP-kinase
cancer, and
encoding a
                                                                      nucleic
                                                                                      factor
                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of tissue
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SO

Sequence

1429

BP; 309

A; 425

G; 220 T; 0 U; 0 Other;

Best Loc Matches

Local

Similarity

100.0%;

Score 44; Pred. No. C; 475

DB 2; 1.2e-11;

Length 1429; Indels

44;

Conservative

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Mismatches

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Query Match

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RESULT 6
ABLO0379/c
ID ABLO03
AC ABLO03
AC ABLO03
AC ABLO03
AX DE Human;
CO Human;
KW Human;
KW Infect
COS Homo s
PN WO2001
XX Homo s
PN WO2001
XX 22-NOV
PR 24-NOV
YX 22-NOV
PR 24-NOV
PR 24-NOV
YX 1Solat
PT Isolat
PT Isolat
PT Isolat
PT POlymc
PR WPI; 2
XX Isolat
PT POlymc
PR WPI; 2
XX Isolat
PT POlymc
PR WPI; 2
XX Isolat
PT POlymc
PR WPI; 2
XX Isolat
PT POlymc
CO Compor:
CC Compor:
CC ABLOO
CC CABLOO
CC CABLOO
CC Subjec
CC ABLOO
CC CABLOO
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                                                                                                                                                                                                                                         ABLOOOIO to ABLOIIO4 represent human nucleic acid oligonucleotides comprising one or more single nucleotide polymorphisms (SNPs). ABB56531 to ABB56903 represent human peptides encoded by some of the SNP coligonucleotides. The sequences from the present invention can have immunosuppressive, cytostatic, antiinflammatory, neuroprotective and antimicrobial activities. Nucleic acids, polypeptides, oligonucleotides and antibodies from the present invention can be used for treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism. The pathology may be autoimmune diseases, inflammation, cancer, diseases of the nervous system, and infection by pathogenic microorganisms. The sure also useful for determining which forms of a characterised colymorphism are present in individuals. The antibodies may be used in the detection, quantitation and/or cellular or tissue localisation of a polymorphic protein (e.g., for use in measuring levels of the polymorphic protein within appropriate physiological samples)
                                                             Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Isolated human nucleic acids comprising one or more single nucleotide polymorphisms, useful for treating a subject suffering from a pathology, e.g. autoimmune diseases, ascribed to the presence of a sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; single nucleotide polymorphism; SNP; polymorphism; cytostatic; immunosuppressive; antiinflammatory; neuroprotective; antimicrobial; autoimmune disease; inflammation; cancer; nervous system disease;
                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-355949/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Page 360; 674pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200138586-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CURA-)
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911 ATGTGGAGCATCGGCGTCATCACCTA 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURAGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RΑ,
                                                                                                                                                                                            51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polymorphic protein;
                                                                                                                                                                                            BP; 11 A; 16 C; 14 G; 10 T;
                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 noncoding SNP oligonucleotide
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                                            2.4%; 50
100.0%; Pre
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                                                          ; Score 26; DB
k; Pred. No. 0.0
0; Mismatches
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                                                                                            DB 5;
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                                                                 0
                                                                                                                           Length 51;
                                                                 Indels
                                                                                                                                                                                                                                                                                         the polymorphic
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                                                             Gaps
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RESULT 8
AAK91856
ID AAK9
XX
AC AAK9
AC AAK9
XX
DT 06-N
XX
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AAX59
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11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of oddy the cDNA. The full libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence was used as the representative sequence from a human clone which was used in homology searches to identify the clone. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from
                                                                                AAK91856;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 757
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su A, Sugiyama T, Nagai
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K, Kojima
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S, Otsuki
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                                                                                                                                                                                                                                                     Human;
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08-JUL-1999;
                                                07-JUL-2000; 2000EP-00114089
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2000JP-00118774.
2000JP-00183765.
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Sugiyama T, Nagai
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K, Kojima
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i T, Koga
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                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                  Human; IFIT-2; chronic myelogenous leukemia; LAGE-1; PIASy; PIASx-alpha; PIASx-beta; DAPK3; gene; ss.
                                                                                                                                                                                                                                                                                                         Nucleotide sequence of human DAPK3
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02-MAY-2000; 2000JP-00183765.
                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                   16-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                    ABV72291 standard; DNA; 2105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
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                       Mano H;
                                                                         01-MAR-2001; 2001JP-00056438
                                                                                                 01-MAR-2002; 2002WO-JP001901
                                                                                                                           12-SEP-2002.
                                                                                                                                                     WO200270747-A1
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                                               (FUJI )
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                                               FUJISAWA PHARM CO LTD
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                                                                                                                                                                                        Location/Qualifiers
94. .1458
/*tag= a
                                                                                                                                                                             /product= "DAPK3"
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a T, Nagai
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Pred. No.
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K, Kojima
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0.016;
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a S, Otsuki
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T, Ko
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WPI; 2002-682911/73

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence encodes human DAPK3. The expression level of the gene is used in the method of the invention. The specification descria a method of examining chronic myelogenous leukemia. The method comprine measuring the expression level of a gene selected from IFIT-2, LAGE-1 BAGE, DDB1, ETS2. PIASY, PIASX-alpha, PIASX-beta and DAPK3, or determining the expression profile of a group of genes including one more of these genes, in a cell or tissue sample from a chronic myelogenous leukemia patient. The method is used for the diagnosis, treatment and prevention of chronic myelogenous leukemia
           The invention provides human and murine recombinant Zipper Interacting Protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine kinases which bind the leucine zipper domain of transcription factor ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic acids are used for the recombinant expression of the proteins. ZIP-kinase protein and DNA are useful as gene therapeutic agents against cancer, and as anti-cancer agents. The present sequence represents a DNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                      Zipper Interacting Prot leucine zipper domain; Human; murine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
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                                                                                                            Claim 5; Page 15-18; 33pp;
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   ZIP kinase
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                                                                                                                                     Zipper Interacting Protein Kinase (ZIP-kinase)
as anticancer agents.
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 protein
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min; transcription
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                                                                                                            English.
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Pred. No.
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on factor ATF4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in a cell or tissue sample for and identification of agents
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Matches 26
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Mezes PS,
Taupier R
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                                 comprising one or more conservative substitutions in the amino acid sequence of (I). The polypeptide is useful for preparing a composition for treating or preventing e.g. cancer. This sequence encodes a death associated protein kinase 3 (DAPK3) interacting protein associated with the identification of novel human proteins and their functions
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24-OCT-2001;
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                                                                                                                           The invention describes an isolated polypeptide comprising any of 33 1273 amino acid sequences (I) given in the specification or its matuue form, a sequence that is at least 95 % identical to (I), or a sequence to the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the contract of the cont
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17-OCT-2001;
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r SR, Gerlach VL, (
PS, Millet I, Ooi
r RJ, Zerhusen BD,
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2001US-0328026P.
2001US-0328056P.
2001US-0328449P.
2001US-0329414P.
2001US-0341058P.
2001US-0341058P.
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2001US-0346357P.
2002US-0391342P.
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Zhong
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Giot L, Gorman L, C
CE, Patturajan M, I
Zhong H, Zhong M;
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Kekuda R;
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Best Local (
                                                                      sequence and an oligonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs and sequences; and sequences; AAB92446 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13639 to AAH13632 represent human amino acid sequences; and AAH13630 to Particularly of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the complete of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
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                                           present invention
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Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ota T, Is
Ishii S,
Senoo C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-OCT-1999;
11-JAN-2000;
17-FEB-2000;
02-MAY-2000;
                                               protein.
fir drug
                                                                                            signalling pathways. Antisense oligonucleotides and compounds ident
by screening (agonists or antagonists) can be used to treat human of
animal disorders associated with the expression or function of the
                                                                                                                                                                                                                                                                                                         New genes encoding protein kinase and protein phosphatase, useful for identifying modulators which can be used to treat human or animal disorders associated with the expression or function of these enzymes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2224
     Sequence 2224
                                                                                                                                                             The present sequence encodes a human protein kinase/protein phosphat The polypeptides are expected to participate in signal transduction cells. The kinase phosphatases are connected with intracellular
                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-564736/63.
P-PSDB; AAG67425.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleotide sequence of a human protein kinase/protein phosphatase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAH78068 standard;
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                                                                                                                                                                                                                                                            1; Page 119-125; 336pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HELIX RES INST
                                               In addition, the polypeptides \overline{\text{may}} be used as target development \dot{}
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Nezu J;
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ilarity 100.0%;
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     ₽P;
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       419
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  A; 656 C; 806 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hikawa T,
Wakamatsu
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A, Nagai 1
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Otsuki
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T, Funahashi S;
                                                                                                                          human or
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Query Match Best Local Similarity Matches 26; Conserv

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                                                    RESULT 16
AAK70641
                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for diagnosing a cancer in a subject. The method comprises determining, in a sample from the subject, the level of at least one polypeptide, where a higher level of the cancer is indicative of cancer. The polypeptide in a subject free of the polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer. The polypeptide is selected from any of the polypeptides. The method of the polypeptides listed in the specification and polypeptides which are at least 70% homologous to the polypeptides. The method of the invention has cytostatic activity, and can year a use in gene therapy. The method is useful in identifying markers specific for one or several types of cancer, depending on the capplications as well as cancer type-specific targets for therapeutic contervention. The compounds that modulate the activity of a tumour content of the present sequence represents a polynucleotide of the invention.
                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Diagnosing cancer comprises determining the polypeptide or polynucleotide levels e.g., hepatic lipase, in a sample from a subject, where a higher level compared to that in a subject free of cancer is indicative of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31-DEC-2002; 2002WO-US041825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human tumour suppressor mRNA SEQ ID NO:228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Feinstein E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (QUAR-)
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AAK70641;
                                      AAK70641 standard;
                                                                                                                                                                                                                                                                                   Sequence 2226 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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26; Conserv
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CLEVELAND CLINIC FOUND.
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                                        DNA; 12638
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  2000US-0231244P
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2000US-0225447P.
2000US-0225757P.
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2000US-0224519P.
2000US-0225213P.
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2000US-0218290P.
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2000US-0180628P
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Matches

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2000US-0233063P. 2000US-0233064P. 2000US-0233065P. 2000US-0234223P.

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RESULT 17
ADB58694
ID ADB58
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08-DEC-2000; 2000US-0251889P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
                            31-JAN-2002;
15-MAR-2002;
15-MAR-2002;
30-DEC-2002;
                                                                                                                                                                                   31-JAN-2003; 2003WO-US003194.
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                                                                                                                                                                                                                                                                                                         WO2003064624-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Toxicity-related gene, SEQ ID 3720.
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                            ; 2002US-00060087.
; 2002US-0364045P.
; 2002US-0364055P.
; 2002US-0436643P.
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                                                                                                                                                                                                                                                                                                                                                                                                                            toxicity assay;
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Pred. No.
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20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000; 08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

08-NOV-2000; 08-NOV-2000; 08-NOV-2000;

08-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

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02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 02-OCT-2000 13-OCT-2000 13-OCT-2000 20-OCT-2000

2000US-0237040P. 2000US-0239935P.

2000US-0237037P. 2000US-0237038P. 2000US-0236369P. 2000US-0236370P. 2000US-0236802P.

2000US-0237039P.

2000US-0240960P. 2000US-0241221P. 2000US-0241785P.

29-SEP-2000; 29-SEP-2000; 29-SEP-2000;

2000US-0236327P. 2000US-0236367P. 2000US-0236368P.

2000US-0235484P.

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RESULT 18
ADB53383
ID ADB53
XX ADB53
XX ADB53
XX D7 04-DE
XX Coxic
XW toxic
XW toxic
XW toxic
XW prima
XX Toxic
XW D7 10-AL
PR 11-AL
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Best Local S
Matches 24
 13-MAR-2002;
13-MAR-2002;
08-APR-2002;
10-APR-2002;
10-APR-2002;
10-APR-2002;
11-APR-2002;
11-APR-2002;
19-APR-2002;
                                                                                                                                                                                                                                                                                              toxic effect; gene expression profile; hepatotoxicity; toxicity marker; toxicity progression; drug screening; primary rat hepatocyte toxicity modelling; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 3720; 1156pp; English
                                                                                                                                                                 04-FEB-2003;
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2002US-0353171P.
2002US-035314P.
2002US-0370248P.
2002US-0371134P.
2002US-0371135P.
2002US-0371150P.
2002US-0371413P.
2002US-0373601P.
2002US-0373602P.
                                                                                                                                                                                                                                                                                                                                                             hepatocyte toxicity modelling related
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Pred. No.
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                                                                                                                                                                                                                                                                                                                               diagnostic marker;
                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO:3925
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30-JUL-2001; 30-JUL-2001;

2001US-00918995

2001US-00918995

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08-MAY-2002;
09-MAY-2002;
09-MAY-2002;
09-JUL-2002;
09-JUL-2002;
09-JUL-2002;
04-SEP-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a method for determining whether a compound induces a toxic effect on a tissue or cell. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising data or information on the Tox mean and non-Tox mean value. The method is useful for predicting or identifying at least one toxic effect, particularly hepatotoxicity, of a test or unknown compound. The genes listed in the specification are useful as diagnostic or toxicity markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound, or to identify or predict the toxic effects of a compound or an agent. These may also be used as markers for monitoring toxicity progression or for drug screening. The present sequence represents a primary rat hepatocyte toxicity modelling related gene sequence from the present invention.
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Elashoff M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
                                                                                                                                                                                                    Human adult brain cDNA #313.
                                                                                                                                                                                                                                                                                        ACH13101 standard; cDNA; 488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2287 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 44; SEQ ID NO 3925; 874pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       642
                                                                                                                                                      ss; sequencing by hybridisation; SBH; expressed mapping; biodiversity; genetic disorder.
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2002US-0378370P.

2002US-0378653P.

2002US-0378655P.

2002US-0394253P.

2002US-0394253P.

2002US-0394253P.

2002US-0407688P.
                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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100.0%; Pred. No.
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RESULT 20
ABZ77137
ID ABZ77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                       Human; protein kinase; enzyme; antiasthmatic; antiinflammatory; antidiabetic; antiparkinsonian; antimigraine; cardiant; cytostatic; antimunosuppressive; vulnerary; gene therapy; COPD; asthma; migraine; chronic obstructive pulmonary disease; non-insulin dependent diabetes; Parkinson's disease; myocardial infarction; inflammatory bowel disease, autoimmune disorder; allograft rejection; graft versus host disease; autoimmune disorder; allograft rejection; graft versus host disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein,
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antisense DNA or RNA.
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(LABA/)
(STAC/)
(DICK/)
                                                                                                                                                                                                                                                                                                                  Human protein kinase encoding cDNA SEQ ID NO:23.
                                                                                                                                                                                                                                                                                                                                                     07-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ77137 standard; cDNA; 1158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seqdata.uspto.gov/sequence.html?DocID=20030073623
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                                                                                                                                         Homo sapiens.
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DICKSON M C.
JONES L W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RT,
                                                                                                                                                                            leukaemia; wound
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LABAT I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CATCGGCGTCATCACCTACAT 205
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                /partial
/product= "protein kinase"
/note= "no start or stop c
                                                                      /*tag=
                                                                                                      location/Qualifiers
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100.0%;
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                start or stop codons given"
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chromosome and gene
or in generating
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ARESULT 21
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ss gene; neuropsychiatric disorder; attention deficit disorder; ADD; schizoaffective disorder; bipolar disorder; unipolar affective disorder; schizophrenia; adolescent conduct disorder; pharmacogenomics; fingerprinting; paternity testing; antidepressant; neuroleptic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   particularly a protein kinase gene agonist or antagonist, can be used for treating a disease or condition associated with a protein kinase in an individual. These diseases include chronic obstructive pulmonary diseases (COPD), asthma, non-insulin dependent diabetes, Parkinson's disease, migraine, myocardial infarction, inflammatory bowel disease, autoimmune disorders (e.g. allograft rejection or graft vs. host disease), cancers
09-JAN-2001;
23-AUG-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK99973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New protein kinase genes and polypeptides, useful for diagnosing diseases associated with a protein kinase, or in gene therapy for treating e.g. Parkinson's disease, migraine, myocardial infarction, allograft rejection
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06-NOV-2001;
                                                                                07-JAN-2002;
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                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                          18-JUL-2002
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2001US-0332870P
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2001US-00935464
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                                                                                                                                                                                                                                                                                                                                                                                                                    CADPKL; ss;
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Best Local S
Matches 21
22-MAY-2001;
13-UUN-2001;
19-UUN-2001;
10-UUL-2001;
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28-AUG-2001;
28-AUG-2001;
27-SEP-2001;
01-NOV-2001;
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                                                                                                                                                                                                                                                            Toxic effect; gene expression profile; renal toxicity; toxicity marker; database; drug screening; toxicity assay; rat; ds.
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                                                                                                                                                   22-MAY-2002;
                                                                                                                                                                                                                                  Rattus norvegicus
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                                                                                                                                                                               28-NOV-2002
                                                                                                                                                                                                                                                                                                     Toxicity modelling related rat gene SEQ ID No 1918
                                                                                                                                                                                                                                                                                                                                  26-JUN-2003
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                                                                                                                                                                                                                                                                                                                                                                                       standard; DNA; 1388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATCGGCGTCATCACCTACAT 939
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2001US-0297235P.
2001US-0297253P.
2001US-0298925P.
2001US-0303807P.
2001US-0303810P.
2001US-0303810P.
2001US-0315047P.
2001US-0330462P.
2001US-0330467P.
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                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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21-FEB-2002;
21-FEB-2002;
15-MAR-2002;
08-APR-2002;
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06-DEC-2001;
19-DEC-2001;
                                                              Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ss; gene; neuropsychiatric disorder; attention deficit disorder; ADD; schizoaffective disorder; bipolar disorder; unipolar affective disorder; schizophrenia; adolescent conduct disorder; pharmacogenomics; fingerprinting; paternity testing; antidepressant; neuroleptic.
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                                                                                                                                                                   Human CADPKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1388 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Organization
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                                                                                                                                                                                                                                   ABK99974;
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2002US-0372794P.
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2002US-0370144P.
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2002US-0357844P.
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No.
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the gene expression
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Best Local
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                                                                                                                                                            Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New variants of calcium/calmodulin-dependent protein kinase-like nucleic acids and polypeptides, useful for diagnosing and treating neuropsychiatric disorders, e.g. schizophrenia, schizoaffective disorder, and bipolar disorder.
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23-AUG-2001;
 26-DEC-2000; 2000WO-US034263.
                                                                 WO200153312-A1
                                                                                              Homo sapiens.
                                                                                                                                              chemokinetic;
                                                                                                                                                                                                                                             Human polynucleotide SEQ ID NO 4692.
                                                                                                                                                                                                                                                                             22-OCT-2001
                                                                                                                                                                                                                                                                                                                                          AAI60703 standard; cDNA; 1956
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                                  26-JUL-2001
                                                                                                                                leukaemia; ss
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DB; ABG69793.
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2001US-00935464
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                thrombolytic; drug screening; arthritis;
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RESULT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                          immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activitys such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and C.N.S disorders. Note: The sequence data for this patent did not form part of the printed specification
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19-OCT-2000;
29-NOV-2000;
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21-JAN-2000;
25-APR-2000;
20-JUN-2000;
19-JUL-2000;
03-AUG-2000;
                                                                           Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
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Wang
Zhou
                                                                 leukaemia; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
            WO200153312-A1
                                        Homo sapiens.
                                                                                                                                                            Human polynucleotide
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                                                                                                                                                                                                                  AAI58917;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and polypeptides, useful for as central nervous system injuries.
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DB; AAM41547.
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Wang Z,
Goodrich
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                                                                                                                                                                                                                                            standard; cDNA;
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ilarity 100.0%;
Conservative
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2000US-00488725.
2000US-00552317.
2000US-00598042.
2000US-00620312.
2000US-00653450.
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2000US-00693036.
2000US-00727344.
                                                                                                                                                                                       (first entry)
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Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                      474 A; 559 C; 508 G;
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                                                                                                                                                               SEQ ID NO 1120.
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Pred. No.
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J, Zhao QA;
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RESULT 26
ADB48899
ID ADB48
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Best Local Similarity
Matches 21; Conserv
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21-JAN-2000; 2000US-00488725.
25-APR-2000; 2000US-00552317.
20-JUN-2000; 2000US-0058042.
19-JUL-2000; 2000US-00620312.
03-AUG-2000; 2000US-00653450.
14-SEP-2000; 2000US-00653936.
19-OCT-2000; 2000US-00693036.
29-NOV-2000; 2000US-00727344.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and constructions. Note: The sequence data for this patent did not form
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous figuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the religious control of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities of the activities 
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                                                                                                                                             Novel human
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P-PSDB; AAM39761.
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                                                                                                             cancer; neurodegenerative disease; human
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Wang Z,
Goodrich
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Wehrman T,
h R, Drmanac
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Xu C,
c RT;
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RESULT 27
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Best Local
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 20-SEP-2000;
02-OCT-2000;
02-OCT-2000;
04-OCT-2000;
10-MAY-2001;
                                                                                                                                                                                                                                                                                                                             Human; cytostatic; antisense gene therapy; screening; protein kinase; cancer; liver; colon; tumour; inflammation; arthritic synovium; CAMK-X1; calmodulin kinase; enzyme; gene; chromosome 1q32.1-32.3; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a polynucleotide comprising a sequence given in the specification, or its mature protein-coding portion, or its complement. The polynucleotide is useful for treating diseases e.g., cancer or neurodegenerative diseases and many others listed in the specification. The present sequence represents a novel human cDNA. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at sequence.html?DocID=20030104529.
                                                                                                                                                                                                                                                 CDS
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                                                                                                          20-SEP-2001; 2001WO-IB002237
                                                                                                                                             28-MAR-2002.
                                                                                                                                                                             WO200224947-A2
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(LIUC/)
(ASUN/)
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25-APR-2000;
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TANG Y T.
LIU C.
ASUNDI V.
DRMANAC R
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Similarity 100.0%; Pred. No.
21; Conservative 0; Mismatc
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2000US-0233999P.
2000US-0237419P.
2000US-0237423P.
2000US-0238558P.
2000US-0290555P.
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2000US-00552317.
2000US-00620312.
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                                                                                                                                                                                                                                             Location/Qualifiers 70. .1500
                                                                                                                                                                                                          /*tag= a
/product= "Human CAMK-X1 protein"
                                                                                                                                                                                                                                                                                                                                                                                                     kinase,
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 The invention relates to a method for screening biologically active agent that modulates cancer associated protein kinase function. The invention CC also relates to a method for diagnosing cancer comprising determining the current converted to the convertion of expression of a nucleic acid sequence encoding a protein CC winase. The method is useful for diagnosing cancer. A protein kinase is cuseful for screening biological agents that modulate cancer associated CC protein kinase function. Downregulating the activity of protein kinase is cuseful for inhibiting the growth of a cancer cell, e.g. liver or colon CC cancer. A nucleic acid encoding protein kinase is useful to screen biopsy CC derived tumours and inflammatory samples such as arthritic synovium, for amplified DNA in the cell or increased expression of corresponding mRNA CC or protein and is also useful to detect differences in expression levels CC such as molecular weight, amino acid and nucleocide sequences between the CC located on chromosome 1q32.1-32.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                             24-FEB-2000;
24-FEB-2000;
24-FEB-2000;
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                                                                                                                                                                                                                                                                                   Human, receptor; diagnostic; therapeutic; gene therapy; vaccine cell proliferative disorder; Crohn's disease; lymphoma; leukaem acquired immune deficiency syndrome; AIDS; autoimmune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16; Page 62-64; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2447 BP; 590 A; 707 C; 604 G; 546 T;
                                                                                                                                                                                                                                                                                                                                                   Human diagnostic and therapeutic polynucleotide (DITHP) #29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAS31014 standard; cDNA; 2689 BP
                                                                                            24-FEB-2000;
24-FEB-2000;
                                                                                                                                               21-FEB-2001;
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                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                       respiratory disorder; ss.
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                              24-FEB-2000;
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2000US-0184693P.
2000US-0184697P.
2000US-018469P.
2000US-0184768P.
2000US-0184769P.
2000US-0184770P.
2000US-0184771P.
2000US-0184771P.
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100.0%; Pre
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Pred. No.
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                                                                                                                                                                                                                                                                                                            leukaemia;
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Chen A, D'sa SA, Amshe
Flores WT, Gre
Roseberry AM, Rosen BH,
Wright RJ, Yap PE, Yu
Cohen HJ, Hodgson DM,
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16-MAY-2000;
16-MAY-2000;
                                                                                                                                                                                                                                                                                                                              Panzer SR, Spiro PA, Banville
Chen A, D'sa SA, Amshey S, Da
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17-MAY-2000;
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15-MAY-2000;
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Fong WT, er.
AM, Rosen BH, Rus
ver, Yu JY,
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2000US-0204863P.
2000US-0205221P.
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2000US-0185216P.
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2000US-0184774P.
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2000US-0205286P.
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2000US-0204821P.
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2000US-0184837P.
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                                                                                                                                                                                                                                                                                              A, Banville SC, Shah P, Chalup MS, Chang SC;
Amshey S, Dahl CR, Dam TC, Daniels SE, Dufour
Greenawalt LB, Hillman JL, Jones AL, Liu TF;
1 BH, Russo FD, Stockdreher TK, Daffo A;
Yu JY, Bradley DL, Bratcher SR, Chen W;
M, Lincoln SE, Jackson S;
                                                                                                                                                                                                                                                                                                                                  Chang SC;
SE, Dufour GE;
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WPI; 2001-502007, P-PSDB; AAU19443. 2001-502867/55.

Polynucleotides encoding diagnostic and therapeutic proteins, e.g. enzymes, hormones and receptors, useful in diagnostics and therapeutics.

Claim 1; Page 310-311; 522pp; English.

cx The invention relates to polynucleotides (I) encoding diagnostic and therapeutic (DITHP) polypeptides (II), which include e.g. enzymes, and CC proteins involved in growth and development and receptors. (I) and (II) may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate DITHP expression. For example, (I) and (II) may be used to treat disorders associated with decreased polypeptide cc expression by rectifying mutations or deletions in a patient's genome, CC that affect the activity of the DITHPs, by expressing inactive proteins or supplementing the patient's own production of them. (I) and (II) may be used to treat diseases, for example, cell proliferative disorder. (CC leukaemia, autoimmune disorders, and respiratory disorders. Additionally, CC (I) may be used to produce the DITHPs, by inserting the nucleic acids in complementary sequences may also be used as DNA probes in diagnostic cassays to detect and quantitate the presence of similar nucleic acids in cassays to detect and quantitate the presence of similar nucleic acids in cassays to detect and quantitate the presence of similar nucleic acids in cassays to detect and and activity. The anti-DITHP antibodies and ancagonists may case describedies may also be used as antigens in the production of cassays to down regulate expression and activity. The anti-DITHP antibodies and ancagonists may case of presence of DITHPs in samples (e.g. by enzyme linked immunosorbant assay (ELISA)). AAS30986-AAS31196 represent human diagnostic and therapeutic complements and samples of the invention

Sequence 2689 BP; 642 A; 748 C; 678 ē, 621 T; 0 U; 0 Other;

Matches Best Local Query Match Similarity 21; Conserv 1.50.08; 51 Score 21; ; Pred. No. Mismatches DB 4; 0; Length 2689 Indels 0 Gaps

RESULT

29

Human

CADPKL

genomic DNA. (first entry) ABK99972;

ABK99972 standard; DNA; 157875

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848

CATCGGCGTCATCACCTACAT CATCGGCGTCATCACCTACAT

868 939

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ABK99972
IID ABK99972
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XX AC ABKX
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                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid comprising a polymorphic region of a Calcium/Calmodulin-dependent protein kinase-like gene (CADPKL) allelic variant, and the polypeptide it encodes. CADPKL allelic variants are useful in determining whether a subject has or is at risk of developing a neuropsychiatric disorder, such as schizophrenia, attention deficit disorder (ADD), schizoaffective disorder, bipolar disorder, unipolar affective disorder and adolescent conduct disorder. The polypeptides, polynucleotides, antibodies and modulators of the CADPKL allelic variants are useful for diagnosting or treating these neuropsychiatric disorders. The polypeptides may be used to raise antibodies to a CADPKL polypeptide. The nucleic acids may be used as probes or primers, in pharmacogenomics for designing therapies for the disorders, and in fingerprinting for detection of different individuals with the same species (e.g. paternity testing). This sequence represents human CADPKL genomic DNA of the invention
                                                                                                                                  Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New variants of calcium/calmodulin-dependent protein kinase-like nucleic acids and polypeptides, useful for diagnosing and treating neuropsychiatric disorders, e.g. schizophrenia, schizoaffective disorder,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; calcium/calmodulin-dependent protein kinase-like gene; CADPKL; ds gene; neuropsychiatric disorder; attention deficit disorder; ADD; schizoaffective disorder; bipolar disorder; unipolar affective disorder; schizophrenia; adolescent conduct disorder; pharmacogenomics; fingerprinting; paternity testing; antidepressant; neuroleptic.
                                                                                                                                                                                                                                                                     Sequence 157875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JAN-2001; 2001US-00757300.
23-AUG-2001; 2001US-00935464.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and bipolar disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meyer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-JUL-2002
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                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Page 119-200;
                                                                                                                                                               Similarity
CATCGGCGTCATCACCTACAT 142389
                                           CATCGGCGTCATCACCTACAT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barrington-Martin R,
                                                                                                                                                                                                                                                                 BP; 44403 A; 35734 C; 34322 G; 43416 T; 0 U; 0 Other;
                                                                                                                       1.9%; bu
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223pp; English
                                                                                                                                                                   Score 21;
Pred. No.
                                                                                                                                  Mismatches
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                                                                                                                                                               DB 6;
                                                                                                                              0,
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Novel purified corn-ear derived polynucleotide useful as hybridization probe for detecting polynucleotide in sample, and for identifying, evaluating, and altering desired characteristics associated with growth,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corn ear-derived polynucleotide; cdp; cDNA library; SATMON022; SA structural gene; functional gene; regulatory gene; corn ear-specific profile; gene transcription; gene expression; hybrid plant; desirable trait expression; plant breeding program; inheritance; desirable trait expression; plant breeding program; disease resistance; environmental adaptability; quality; yield;
                                                                                                                                                                                                                                                                   Example;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABX87988 standard; cDNA; 295
                                                                                                                                                                                                                                                                                                                                       WPI; 2003-208840/20
                                                                                                                                                                                                                                                                                                                                                                                                 26-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                   14-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zea mays.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                multigene
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                                                                                                                                                                                                                                                                                                                                                         RV,
                                                                                                                                                                                                                                                                                                                                                                             INCYTE
                                                                                                                                                                                                                                                                  SEQ ID NO 6448; 390pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               trait; plant; gene; ss.
                                                                                                                                                                                                                                                invention relates to the isolation
                                                                                                                                                                                                                                                                                                                                                         Ito LY,
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                                                                                                                                                                                                                                                                                                                                                                             GENOMICS INC
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                                                                                                                                                                                                                                                                                                                                                         Sherman
                                                                                                                                                                                                                                                                                                                                                         BK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #6448
                                                                                                                                                                                                                                      of corn ear-derived
) cDNA libraries SAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SATMON022; SATMON023;
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CC polymoreotides (cdps) from the corn (Zea mays) cDNA libraries SATMON022
CC and regulatory genes of corn ear. The polymorelectides sequences are cc useful for detecting cpds in a sample, for producing a corn ear-specific profile of gene transcription, for detecting altered gene expression in continued or hybrid plants, and for screening several molecules for specific binding to the polymorelectide. The cdps are useful to identify, isolate, or extend identical or related corn-ear mucleic acid sequences from DNA cc libraries, and in mucleic acid amplification or hybridisation techniques to follow the expression of desirable traits through plant breeding corpograms. Preferably, the cdps are useful to identify, evaluate, or cf follow the inheritance of desired characteristics associated with growth can development, disease resistance, environmental adaptability, quality, and yield of corn. The cdps are also useful as molecular markers for studying inheritance and multigene traits in a plant breeding program. The cpds are useful for producing purified corn-ear polypeptides by crecombinant techniques. They are also useful in diagnostic assays to of cdp expression. ABX81541-ABX89140 represent corn car-derived corpositions conditions or diseases associated with abnormal levels of cdp expression. ABX81541-ABX89140 represent corn car-derived corn part of the printed specification, but was obtained corn electronic format directly from the USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html

Sequence 295 BP; 62 A; 83 C; 104 G; 45 T; 0 U; 1 Other;

Query Match Best Local Matches Local Similarity 100.0%; 1.88: <u>.</u> Score 20; Pred. No. Mismatches DB 7; Length 295; Indels 0

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RESULT 32
AAI38308
ID AAI38
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AC AAI38
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DT 17-OC
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DE Probe
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Matches 20
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                     The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human foetal liver single exon nucleic acid probe
                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200157277-A2
             Probe #6994 used to
                                  17-OCT-2001
                                                                           AAI38308 standard; DNA; 447
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 6939; 639pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (MOLE-)
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                                                                                                                                                                                                                                                                                                                                                            expression
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                                                                                                                                284
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                                                                                                                                                                                                                                                                                                                                                           genome-derived single exon nucleic acid probes useful expression in human fetal liver.
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                                                                                                                                                                                   Similarity
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                                                                                                                                TGATCTTGGAGCTGGTGTCC 303
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2000US-00638408.
2000US-00632366.
2000US-02346879.
2000US-0236359P.
2000GB-00024263.
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              measure
                                  entry)
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            gene
                                                                             ВP
                                                                                                                                                                          0;
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Pred. No.
                                                                                                                                                                                                                   74 G; 138 T; 0 U; 0 Other;
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            expression in
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            human placenta sample
                                                                                                                                                                                               Length 447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid probe;
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RESULT 33
AAK32477
ID AAK32
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Best Local
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26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probe; microarray; human; placenta; antenatal diagnosis;
genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                       Sequence 447 BP; 95 A; 140 C; 74 G; 138 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to single exon nucleic acid probes The probes are useful for predicting a microarray for predicting, measuring and displaying expression in samples derived from human placenta. The probes are for antenatal diagnosis of human genetic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Penn
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-AUG-2001.
                                                                                                                                    Human; bone marrow expressed exon; gene expression analysis; probe;
microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                 Human bone marrow expressed single exon probe SEQ ID NO:
                                                                                                                                                                                                         AAK32477;
                                                                                                                                                                                                                            AAK32477 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                                                                                      06-NOV-2001
                                                         30-JAN-2001; 2001WO-US000668
                                                                             09-AUG-2001.
                                                                                                WO200157276-A2
                                                                                                                   Homo sapiens
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; 2000US-0180312P.
; 2000US-0207456P.
; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
                                                                                                                                                                                                                                                                                                                   Conservative
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2000US-0236359P.
2000GB-00024263.
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2000US-00608408.
2000US-00632366.
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                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        in human placenta.
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Pred. No.
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18;
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are useful
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RESULT 34
AAK06764
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Best Local :
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-0060840B.
03-AUG-2000; 2000US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236559P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cances such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .83
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                 Example
                                                                              Single
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04-OCT-2000;
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                 4;
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                                                                                                                                                                                                         MOLECULAR DYNAMICS INC
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2000GB-00024263.
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                 6755;
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Pred. No.
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                 + Sequence Listing;
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Best Local S
Matches 20
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                                                                             The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be
involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which associated with coronary heart disease. ABS25011-ABS51005 represent hun liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                      Penn
                                                                                                                                                                                                                                  Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-AUG-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; single exon nucleic acid probe; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia; coronary heart disease; ss.
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                                                                                                                                                                                          Claim
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27-SEP-2000;
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2000US-0207456P.
2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0234359P.
2000US-00024263.
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RESULT 36
ABS07263
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Best Local
The invention relates to a spatially-addressable set of single exon nucleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of 12614 nucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung; measuring gene expression in a sample derived from human lung; comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interstitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; cuberous sclerosis; Gaucher's disease; Niemann-Pick disease; tuberous sclerosis; Gaucher's disease; Niemann-Pick disease; pulmonary histocytosis; lymphangioleiomyomtomary haemosiderosis; pulmonary histocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; primary ciliary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 447 BP; 95 A; 140 C; 74 G; 138 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                 WPI; 2002-114183/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000;
26-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genome-derived single exon probe from lung
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                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                    measure
                                                                                                                                                                                                                                                                                  Spatially-addressable set of single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                  Penn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JUN-2000;
03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hyaline membrane disease.
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                                                                                                                                                                                                                                                                                                                                                                                   (MOLE-)
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20; Conservative
                                                                                                                                                                                                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                   MOLECULAR DYNAMICS
                                                                                                                                                                                                                                   SEQ ID NO 7254; 634pp; English.
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2000US-00608408.
2000US-00608408.
2000US-00632366.
2000US-023468-P.
2000US-0236359P.
2000US-0206324263.
                                                                                                                                                                                                                                                                 expression in human lung samples.
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Pred. No.
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                                                                                                                                                                                                                                                                                  probes, used
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the eukaryote; and (b) detecting specific hybridisation of detectably comparison of a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in several ctissues and/or cell types using hybridisation to a single gene capression of the exons single sene; a period to the exons should be assigned to a single exon comprising one compression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single eyen; a period comprising one of 12011 sequences, mentioned in the specification, or encoded by the probee/open reading frames (ORF). The probes are used for gene expression compression and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as asthma, lung cancer, chronic obstructive pulmonary disease (CODP), interstitial lung cancer, chronic obstructive pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-puldisk syndrome, sarcoidosis, pulmonary haemosiderosis, pulmonary critary compared to a single exon probe of the primary ciliary dyskinesis, pulmonary haemosiderosis, pulmonary ciliary compared data for this patent did not form part of the printed case expression and hyaline membrane disease. The specification, but was obtained in electronic format directly from WIPO as formators.
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Best Local
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genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 447 BP; 95 A; 140 C; 74 G; 138 T; 0 U; 0 Other;
                                                                                                                                              (LABA/)
(STAC/)
(DICK/)
                                                                                                                                                                                                                                                                                                17-APR-2003
                                                                                                                                                                                                                                                                                                                                US2003073623-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human mammary gland cDNA #232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACH50827 standard; cDNA; 493 BP
                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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                                                             WPI; 2003-615964/58.
                                                                                                                                                                                             (DRMA/)
                                                                                                                                                                                                                                                             30-JUL-2001; 2001US-00918995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ftp.wipo.int/pub/published_pct_sequences
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20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             ss, sequencing by hybridisation, SBH; expressed sequence tag; mapping, biodiversity, genetic disorder.
                                                                                                                           STACHE-CRAIN
DICKSON M C.
JONES L W.
                                                                                              RΤ,
                                                                                                                                                                                             DRMANAC R T.
                                                                                                                                                                               LABAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATCTTGGAGCTGGTGTCC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGATCTTGGAGCTGGTGTCC 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ilarity 100.0%;
Conservative
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                                                                                             Ħ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.8%;
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Pred. No.
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                                                                                                Dickson MC,
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                                                                                                                                                                                                                                                                                                                                                                                                                    EST;
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New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating

DNA

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RNA

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RESULT 38
AAT17177
ID AAT17
XX AAT17
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XX KM-02
XX KM-02
XX KM-02
XX KM-02
XX Rhodo
XX Rhodo
XX CDS
FT CDS
FT CDS
FT CDS
FT CDS
FT CDS
XX AAT17
XX AAT17
XX KM-02
XX KM-02
XX KM-02
XX Rhodo
XX AP7
PR 04-AU
XX 01-AU
XX NT F,
XX WP1;
PR WP1;
PR P-PSD
XX Rhodo
PT CONst
XX Claim
XX Claim
XX Claim
XX Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, CC informatics, in assessing biodiversities, or in identifying mutations CC responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, CC for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data contained in electronic form part of the printed specification, but was cobtained in electronic format directly from USPTO at sequence.html?Doc1D=200100774673
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                                Claim 2; Page 10; 15pp;
                                                                      Rhodococcus sp. construction of
                                                                                                                         P-PSDB;
                                                                                                                                                                              Yu F,
                                                                                                                                                                                                                                                   04-AUG-1994;
                                                                                                                                                                                                                                                                                     04-AUG-1995;
                                                                                                                                                                                                                                                                                                                           03-APR-1996.
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                                                                                                                                                                                                                 ) NITTO CHEM IND CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain;
                                                                                                                                                                              Kato M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rhodochrous.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kanamycin resistance gene; marker; construction; system; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                   94JP-00201582.
                                                                                                                                                                                                                                                                                       95EP-00112298
                                                                  Kanamycin resistance gene self-cloning systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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                                  English
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Pred. No.
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    useful

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The present

sequence

is the R. rhodochrous,

strain

KM-02,

Sequence 1120 BP;

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304 C;

315 G;

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XXX ABA0
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Best Local
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23-AUG-2000;
30-NOV-2000;
                                                                            and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, centra and peripheral nervous system diseases and neuropathies, such as Alzhelmer's, Parkinson's and Huntington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New bone marrow-expressed nucleic acids and polypeptides, useful for diagnosis, treatment of inflammatory, autoimmune, neurological, cance and increasing hematopoiesis, stem cell survival and bone growth and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tang
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       resistance gene, useful as a marker in the construction of a self cloning system, pref. for the self cloning of R. rhodochrous. Only the CDS of the gene is claimed, however the the entire gene sequence is referred to in example 1 of the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAR-2001; 2001WO-US010472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nervous system disorder; autoimmune disorder; inflammation; allergy; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human bone marrow expressed oligonucleotide SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 748 BP; 138 A; 240 C; 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-0CT-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABA09608 standard; DNA; 1120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic;
antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;
immunostimulant; analgesic; cerebroprotective; antianaemic; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-JAN-2002
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                                                                                                                                                                                                                                                                                                                                present invention relates to bone marrow expressed polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-626375/72.
DB; ABB12364.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   658 ACATCATGTTGCTGGACAAG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bone marrow; cytostatic; antirheumatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                        Page 182; 380pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATCATGTTGCTGGACAAG
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2000US-00649167.
2000US-0250583P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ·.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ford JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boyle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer
h and
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RESULT 41
AAS73461
ID AAS73
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AC AAS73
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ADA69943
ID ADA69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                           Query Match
Best Local &
                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                             The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant; bacterial infection; fungal infection; viral infection; rice
     AAS73461;
                                      AAS73461 standard; cDNA; 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pathogenic infection bacterial, fungal or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chang H, Cl
Katagiri F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2003
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                                                                                                                                                                                                                                                                 Sequence 1130 BP; 272 A; 305 C; 303 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-175290/17.
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                                                                                                                                                                                                                                                                                                  illustrate
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                                                                                                                                                                                             l Similarity
20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chen w, Quan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGTCATCACCTACATCCT 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 3266; 899pp; English.
                                                                                                                                                            TCCGCCACCCCAACATCATC 459
                                                                                                                            TCCGCCACCCCAACATCATC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID 3266.
                                                                                                                                                                                                                                                                                                  the invention.
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                                                                                                                                                                                           1.8%; Scilarity 100.0%; F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cooper B, S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           one gene involved in plant resistance or response for conferring resistance or tolerance to a plant viral infection by determining or detecting plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                               Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
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Pred. No.
                                        BP
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18;
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د.
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ID AAC
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DT 18
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                                                                                                                                                                                                                                                                                                                                                cc sequences. (I) is useful as hybridisation probes, polymerase chain cc reaction (PCR) primers, oligomers, and for chromosome and gene mapping, cc and in recombinant production of (II). The polymerase chain cc in diagnostics as expressed sequence tags for identifying expressed cc genes. (I) is useful in gene therapy techniques to restore normal cc activity of (II) or to treat disease states involving (II). (II) is cusful for generating antibodies against it, detecting or quantitating a cc gulypeptide in tissue, as molecular weight markers and as a food cusful for generating antibodies against it, detecting or quantitating a cc gulypeptide in tissue, as molecular weight markers and as a food conjugation of sites expressing (II). (I) and (II) are useful in medical imaging conjugation approach expression or biological activity. The cc gulypeptide and polymucleotide sequences have applications in conjugations, forensics, gene mapping, identification of mutations cc gand to produce other types of data and products dependent on DNA and camino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this cated and product of the invention. Note: The sequence data for this cated are conjugated and conjugated activity from willout from introview for his printed specification, but was obtained in celectronic format directly from willout.
                                                                                                              RESULT 42
                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; forensic;
food supplement; medical imaging; diagnostic; genetic disorder;
           18-OCT-2000
                                                                                                                                                                                                                                                                                                     Sequence 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 9265; 103pp; English.
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23-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention
                                            AAC46591;
                                                                             AAC46591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                        ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                 324
                                                                                                                                                                                                  382
                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                    Similarity
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	<pre>fragment SEQ ID NO: 50700.  assay; genetic mapping; gene expression control; ification; signal transduction pathway; metabolic; pathway; rmination sequence; corn; ss.</pre>
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31-AUG-1999;
01-SEP-1999;
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Human; bone marrow; cytostatic; antirheumatic; antiarthritic; vulnerary; antiinflammatory; antibacterial; immunosuppressive; vasotropic; cancer; antiparkinsonian; neuroprotective; nootropic; haemostatic; osteopathic; antiulcer; fungicide; antidiabetic; antiasthmatic; antiallergic;
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                                                                                                            Human bone marrow expressed oligonucleotide SEQ
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23-AUG-2000;
30-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to bone marrow expressed polynucleotides and proteins. These sequences can be used in the treatment of inflammatory conditions (eg arthritis, Crohn's disease), cancer, central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's and Huncington's diseases, spinal cord disorders, head trauma, cerebrovascular diseases, myeloid and lymphoid cell disorders, platelet disorders, stem cell disorders, bone degenerative disorders, autoimmune disorders, for example multiple sclerosis, diabetes and arthritis, viral and bacterial infections, allergies and blood coagulation disorders. The present sequence is a DNA
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                                                                                                                                                                                                                    DAP-kinase-related protein 1; DRP-1; Death-Associated Protein; calmodulin-dependent serine/threonine kinase; apoptosis; dimerisation; cytostatic; antipsoriatic; immunosuppressive; metastasis; tumour; humacytostatic; immunosuppressive; metastasis; immunosuppressive; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; metastasis; me
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and increasing hematopoiesis,
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nervous system disorder; autoimmune disorder; inflammation;
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cancer; psoriasis; autoimmune
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RESULT 45
AAV49655
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                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence encodes DAP (death-associated protein) - kinase-related protein 1 (DRP-1), which is a calmodulin-dependent serine/threonine kinase. DRP-1 is a cytoplasmic protein capable of inducing apoptosis by dimerisation. It shows significant homology to DAP kinase. It has cytostatic, antipsoriatic and immunosuppressive activity and can be used for inhibiting growth/metastasis of tumours and promoting death of tumour cells. It can also be used in the treatment of cancer, psoriasis and autoimmune diseases. Fragments of DRP-1 DNA are useful as probes for screening individuals with a predisposition to cancer
                                                                                                                                                                                       Scavenger receptor cysteine rich domain; SRCR; diagnosis; treatment; nervous system; medullo-blastoma; glioma; breast; detection; SC3; autoantibody; ss.
                                                        09-JAN-1997;
18-JUL-1997;
                                                                                            09-JAN-1998;
                                                                                                                                          WO9830687-A2
                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                       Human
                                                                                                                                                                                                                                                               23-OCT-1998
                                                                                                                                                                                                                                                                                      AAV49655
                                                                                                                                                                                                                                                                                                            AAV49655 standard; DNA; 28720 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1742 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 3; Fig 1; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis used in the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Calmodulin-dependent serine/threonine kinase capable of inducing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY44674.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-147148/13.
            Mollenhauer
                                                                                                                   16-JUL-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kimchi A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1998;
                                  (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (YEDA ) YEDA RES & DEV CO LTD (MCIN/) MCINNIS P A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-1999.
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                                                                                                                                                                                                                                                                                                                                                                        215
                                                                                                                                                                                                                                                                                                                                                                                            382 AGCCGGCGCGGTGTGAGCCG 401
                                                                                                                                                                                                                                       SC3 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                       AGCCGGCGCGGTGTGAGCCG 234
          4
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                             (first entry)
                                                        97DE-01000519.
97DE-01030997.
                                                                                           98WO-DE000096
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  442 A; 437 C; 504 G; 359 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                 1.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of e.g. cancer.
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1742;
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Search completed: June 30, 2004, 19:02:41 Job time : 512 secs

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В
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                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This nucleotide sequence contains a fragment of a gene which is capable of encoding a protein which contains a SRCR (scavenger receptor, cysteinn rich) domain. The gene and encoded protein can be used to diagnose or treat tumours, particularly of the nervous system (medullo-blastoma or glioma) or breast. The DNA sequence and probes derived from it, are used to identify genes that express SRCR-domain containing proteins, to determine the form in which these proteins exist and to assess the significance of individual forms on cellular properties. The protein can be used to detect the presence of autoantibodies and antibodies which
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 28720 BP; 6956 A; 6728 C; 6982 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins containing scavenger receptor, diagnosis and treatment of tumours.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-399136/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 5c; 54pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulate its expression
     22565
                                                                                             952 TGAGATGGGCAGGGGCCTCA
TGAGATGGGCAGGGGCCTCA
                                                                                                                                                                                                Conservative
                                                                                                  1.8%; Fred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. No. 100.0%; Pred. 
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در
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Perfect
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -MODEL=frame+_p2n.model -DEV=xlh
-Q=/cgn2 1/USPTO_spool/GEREXESUS641/runat_29062004_143151_24560/app_query.fasta_1.519
-DB=GenEmbl -OpMT=fastap_ -SUFFIX=rye -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DCCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALIGN=15 -MCDE=LOCAL
-OUTPMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=GEBREYESUS641_@CGN 1_1_3508_@runat_29062004_143151_24560 -NCPU=6 -ICPU=3
-NO_MAAP -LARGEQUERY -NEG_SCORES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEDUT=120 -MARN_TIMEDUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-DEV_TIMEDUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
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DB seq length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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1826
1 XMXIGLIGRSSPXGQLDSLS......GXEMSLGTLDMPGPHQXRTX 361
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Maximum Match 100%
Listing first 45 summaries
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29: em vi: *
30: em htg hvm: *
31: em htg lnv: *
32: em htg lnv: *
33: em htg lns: *
34: em htg ln: *
36: em htg ln: *
36: em htg ln: *
37: em htg mam: *
37: em htg vri: *
39: em htg vri: *
40: em htg omus: *
41: em_htgo_other: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

## Result റ റ No. 1513.5 1513.5 1513.5 631.5 930 858.5 876.2 722 722 722 632 632 632 6332 6332 Score 632 84.0 214000 82.9 2188117 82.9 246796 450.9 247196 46.9 11514 39.5 11410 39.5 11429 34.6 2079 34.6 2105 Match Length 10 10 10 10 10 6 9999999 00000 AC120292 AC114704 AC014643 AC093823 AC0073822 ) BC062076 ) RNO6971 ) AR0697143 AR0761190 AR124103 E23385 AK027590 AK097643 BD124885 BD126291 AC0134201 AC013577 AB018001 AF052941 BC022165 BY245541 AY245541 AY245541 AY245541 AY245541 AY245541 AY245541 BC057317 BC060161 BX539340 AB022341 BD127287 AK074799 BD176607 AB007144 AR076189 AR124102 E23384 AX880020 BD012208 BD158150 AY335738 AK027590 Homo sapi AK097643 Homo sapi BD124885 Primer fo BD126291 Primer fo AC034201 Homo sapi AC011488 Homo sapi AC113577 Tetraodon AB018001 Homo sapi AF052941 Homo sapi BC022165 Mus muscu AY245540 Mus muscu AY245540 Mus muscu BC057317 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu BC060161 Mus muscu AB022341 Homo sapi BD127287 Primer fo AK074799 Homo sapi BD176607 Method of AB007144 Homo sapi AR076189 Sequence AR124102 Sequence E23384 DNA encodin AC120292 Rattus no AC114704 Rattus no AC094643 Rattus no AC073822 Mus muscu X76104 H.sapiens D BD193362 Compositi AR080622 Sequence AB018002 Mus muscu BT006935 Homo sapi BT007780 Synthetic AX880020 Sequence BD012208 Novel gen BD158150 Primer fo AR076190 Sequence AR124103 Sequence E23385 DNA encodin Description BC062076 Rattus no AJ006971 Rattus no AB007143 Mus muscu AY335738 Synthetic

ALIGNMENTS

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                                                                                        Submitted (05-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 240009)
                                                                                                                                                                                                                                                                                                                 Worley, K.C.
Direct Submission
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                             FIGURE9 (1-361) x AC120292 (1-240009)
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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                   Alignment Scores:
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                                                                                                                                                                                                                                                                                                                                                                                                 misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hggc.bcm.tmc.edu/docs/Genbank draft data.h NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
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Center clone name: CH220-239B15
Center clone name: CH220-239B15
Center clone name: CH220-239B15
Center clone name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 207207 bases at least Q40
Consensus quality: 208683 bases at least Q20
Consensus quality: 208684 bases at least Q20
Estimated insert size: 213125; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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Center: Baylor College of Medicine
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/clone="CH230-239B15"
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715	CCCCTAACTGTTCCCAACCTGTGGGCCTTATTCAGCTAGTGAGGGTGTGGGGCCCTAGACA 2147:	214656	дb
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55	GlyHisHisProIleGly***IleLeuHisGlyLeuGlyLeuThrCysLeuAsnAsnPr 282 	262 s   214476 T	당 성
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35 5	**SerArgArgThrSerCysCysTrpTh 222 	213 - 214296 A	B &
295	THEMINE	214236 (	B 45
23 5	ArgSerSerSerSerArgSerTrpThrValSerThrThrCysThrProSerAlase 208	76	Q 09
175	gMetAr 188       GATGAG 2141	a a	D S
L15	lelleThrLeuHisAspValPheGluAsnLysThrAspValValLeuIleLeuGluLeu 168 	149 I   214056 A	DB QY
)55 5	ValSerArgGluGluIleGluArgGluValSerIleLeuArgGluIleArgHisProAsn 148 	6 9	B 8
995	GlyMetGluTyràlaAlaLysPheIleLysLysArgArgLeuProSerSerArgArgGly 128	6 9	B 8
ម មា	CysSerPheProHisSerGlyPheAlaIleValArgLysCysLysGlyThr 108	92 ( 213876 :	B 8
375	hraspalaGlnargLeuGlyTyrargValLeuProSerSerGlySerAlaAlaLeuSer 91 	72 T   213816 A	B 8
57	leProLysCysLeuSer***GlySerLeuGlySerSerValValValGlyAsnLeuGly 71 	52 I   213756 A	B 8
755	AsnLeuThr***LeuPheLeuGlyProArgCysArgAlaSerValLeuSerLeuLysAla 51	32 <i>}</i> 213696 <i>}</i>	8
595	ro****GlyGlnLeuAspSerLeuSerAspLeuLeuLeuSerArgProGlnHisGlyIle 31 	12 P       213636 C	40

RESULT 2 AC114704/c LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS	g &	g Q	d Qy	90	р В	γ	DЪ	γQ	Db
SULT 2 Ili4704 AC1147	343 *GluMetSerLeu-GlyThrLeuAspMetPro 353    :::	323 lProAlaArgGlyProGlyIleArgAlaGlyThrSerAlaAsnCysLysHisTrpGly** 343 	303 uHisArgArgHisHisLeuHisProValSerAla***AspGlyGlnGlyProGlnThrVa 323	N	TGCCCAGGTGCTCAGGCAACCCTGTGGTTGACACTGACAACACCCTAGAGTGGGGCCCTA	302	214776 TGCTCAGTCACACGGGGCTTGCTGTCGTCGGATAGGGTTCTGAGGTTCTGCTGTCCTGGC 214835	302 302	214716 GCAGCATGGAAGGGCTGAGACCCCCTGCTCAGACCCCAACCTATCAGACTACATGGGCTC 214775

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Puzzó, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sheed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Walliams, G., Willson, R., Wleczyk, R., Weden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, X., Zhao, S., Dunn, D., Yon, Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:23265882.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlass (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Submitted (11-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 218817)
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is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 218817: contig of 218817 bp in length.

Location/Qualifiers
                                                                                                                                                                                                                                   NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft data./NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: GSBS
Center clone name: CH230-55A15
Center clone name: CH230-55A15
Center clone name: CH230-55A15
Center clone name: CH230-55A15
Center clonery Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 207315 bases at least Q40
Consensus quality: 209091 bases at least Q30
Consensus quality: 210263 bases at least Q20
Estimated insert size: 213462; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 218817)
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DB:
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Best Local Similarity:
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FEATURES

source

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122514 AACCTCACTTGACTGTTCTTGGGTCCCCGGTCCCGGCCAGCGTCCTCTCCCCTCAAGGCA 122455
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rSerMetG1nProAlaHisAlaLeuSerSerSerThrLeuAlaSerArgThrG1ySerAr
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ValSerGlyGlyGluLeuPheAspPheLeuAlaGluLysAsp-His***GlnArgMetAr 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GlyMetGluTyrAlaAlaLysPheIleLysLysArgArgLeuProSerSerArgArgGly 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleProLysCysLeuSer***GlySerLeuGlySerSerValValValGlyAsnLeuGly 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pro***GlyGlnLeuAspSerLeuSerAspLeuLeuLeuSerArgProGlnHisGlyIle 31
                                                                                                                                                                                                GCGCACTTTGACCTGAAGGTAGCTTGTGTGAGTGGGCGTGGGGAAGGGAAGGGCAGGGATA 121915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTGAGCCGTGAGGAGCTCGAGCGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAAC 122155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ValSerArgGluGluIleGluArgGluValSerIleLeuArgGluIleArgHisProAsn 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATCCCCAAGIGICIGICATGAGGCICITIGGGCAGTICIGITGITGIGGGAAACCIGGGA 122395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IleIleThrLeuHisAspValPheGluAsnLysThrAspValValLeuIleLeuGluLeu 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGTTCCTTCCCCACAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGATGCACAGAGGCTGGGGTACAGAGTCCTGCCTTCCTCTGGGTCTGCAGCGCTTAGC 122335
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                                                                                                                                                                                                                                                                                                                 GCCACGCAGTTCCTCAAGCAGATCCTGGACGGTGTCCACTACCTGCACTCCAAGCGCATC
                                                                                                                                                                                                                                                                                                                                                                 gProArgSerSerSerSerArgSerTrpThrValSerThrThrCysThrProSerAlaSe 208
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217464. .217908
/note="clone_boundary
clone_end:Sp6
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/db_xref="taxon:10116"
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66.26%
82.89%
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Matches:
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                                                                                                                                  --***SerArgArgThrSerCysCysTrpTh
                                      242
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                                                                                                                                                                                                                                                                                                                    121975
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Db 1218	54 AAGCATGCAGCCAGCCCACGCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAG 121795
Qy 2,	42 gProValAlaSerSerArgThrSerLeuAlaArgGlnSerSerSerValArgGlyArgCy 262
Db 12179	94 GCCGGTAGCGAGTTCAAGAACATCTTTGGCACGCCAGAGTTCGTCGGTGAGGGGCAGGTG 121735
Оу 26	sHisProIleGly***IleLeuHisGlyLeuGlyLeuThrCysLeu
Db 12173	GGCACCACCCGATAGGGTAGATTCTGCACGGCCTTGGCCTGACCTGCCTCA
Фу 28	sLysLeu***ThrThrTrp
Db 1216:	lácici organization de la composição de
ΩУ 30	02 1 302
Db 12161	14 -GGTGAGTGGGGTTGGCAGAGGCCCTGCCCTGCTCCATTCTCTCCCGTGCTTCCCGTGCT 121556
Qy 30	02 302
Db 1215	55 CCCCTAACTGTTCCCAACCTGTGGGCCTTATTCAGCTAGTGAGGGTGTGGGGCCCTAGACA 121496
Ωу . 30	02 302
Db 12149	95 GCAGCATGGAAGGGCTGAGACCCCCTGCTCAGACCCCAACCTATCAGACTACATGGGCTC 121436
Ωу 3(	02 302
Db 12143	35 IGCTCAGTCACACGGGGCTTGCTGGTCGTCGGATAGGGTCCTGAGGTTCTGCTGTCCTGGC 121376
Ωу з(	02 302
Db 1213:	75 TGCCCAGGTGCTCAGGCAACCCTGTGGTTGACACTGACAACACCCTAGAGTGGGGCCCTA 121316
Qy 30	03G1 303
Db 12131	15 TGTCCTGGGGTGGAGTGCTGCCAAGGCCATTCTGACCAGACTTTTCTGCCCCTTTGCAGGA 121256
. ω	3 uHisArgArgHisHisLeuHisProValSerAla***AspGlyGlnGlyProGlnThrVa 323
מם בצוצו	ATUGGUGTUATUACUTACATUUTGIGAGTIGUUTGAGATGGGGAGGGGGCTCAGACTG
Qy 3:	ProAlaArgGlyProGlyIleArgAlaGlyThrSerAlaAsnCysLysHisTrp
Db 1211	CTGCTAGAGGCCCAGGGATCAGGGCTGGCACCTCTGCAAACTGCAAACA
Qy 34 Db 12113	43 *GluMetSerLeu-GlyThrLeuAspMetPro 353    :::
RESULT 3 AC094643/c LOCUS DEFINITION	AC094643 AC094643 AC094643 AC094643 AC094643 ACOPACT SEQUENCE, 3
ACCESSION VERSION KEYWORDS SOURCE ORGANISM	PHAS PHAS rvegi rvegi Euth
REFERENCE AUTHORS	r,M.Lee., Abramzon,S., Adams,C., Alder,J., Abrooks,S., Amin,A., Anguiano,D., A., Ayodeji,M., Baca,E., Baden,H., A., Ayodeji,M., Barnstead,M., Benahmed, Blankenburg,K., Blyth,P., Brown,M., Brich,P., Burrell,K., Calderon,E., Cavazos,I., Ceasar,H., Center,A., Chen,G., Chen,R., Chen,Z., Chu,J.
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Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dhinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fraser, C.M., Galisi, A., Ganta, R., Garcia, A., Garner, T., Gazza, M., Guerra, W., Guerra, W., Gunaratne, P., Haland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, M., Hernandez, J., Hernandez, R., Hines, S., Hladkin, S.L., Hodgson, A., Hoglus, M., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Idlebitd, D., Jackson, A., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Liu, J., Liu, W., Liu, Y., London, P., London, P., Longacre, S., Lopez, J., Liu, J., Louiseged, H., Lozado, R.J., Lu, X., Mad., Maheshwari, M., Mahindartne, M., Mathin, R., Martin, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Socat, R., Martin, R., Wat, X., Mhite, F., Mang, J., Martin, J., Wath, R., Martin, R., Wat, R., Martin, R., Martin, R., Martin, R Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24818455.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represented as scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that cone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 246796)
Rat Genome Sequencing Consortium. shotgun sequence only contigs will be indicated in the feature table. Worley, K.C. Direct Submission Direct Submission Unpublished
2 (bases 1 to 246796) Direct Submission Genome Center

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NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of grapes are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                    IleProLysCysLeuSer***GlySerLeuGlySerSerValValValGlyAsnLeuGly
                                                                                                                                                                                                                                                       AsnLeuThr****LeuPheLeuGlyProArgCysArgAlaSerVaiLeuSerLeuLysAla
                                                                                                                                                                                                                                                                                                           Pro***GlyGlnLeuAspSerLeuSerAspLeuLeuLeuSerArgProGlnHisGlyIle
                                        CysSerPheProHisSerGly---PheAlaIleValArgLysCys-----LysGlyThr
                                                                                        ACAGATGCACAGAGGCTGGGGTACAGAGTCCTGCCTTCCTCTGGGTCTGCAGCGCTTAGC
                                                                                                             ThrAspAlaGlnArgLeuGlyTyrArgValLeuProSerSerGlySerAlaAlaLeuSer
                                                                                                                                                             ATCCCCAAGTGTCTGTCATGAGGCTCTTTGGGCAGTTCTGTTGTTGTGGGAAACCTGGGA
                                                                                                                                                                                                                                    AACCTCACTTGACTGTTCTTGGGTCCCCGGTGCCGGGCCAGCGTCCTCTCCCTCAAGGCA
                 TGTTCCTTCCCCACAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACC
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Consensus quality: 227791 bases at least Q40
Consensus quality: 230373 bases at least Q30
Consensus quality: 230366 bases at least Q30
Consensus quality: 232066 bases at least Q20
Estimated insert size: 237543; sum-of-contigs estimation
Quality coverage: 8x in Q20 bases; sum-of-contigs estimation
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Center clone name: CH230-5B18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             end_sequence:BH334507"
complement(241125..241693)
/note="clone_boundary
clone_end:T7
site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-5B18"
10347. .199080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                end_sequence:BH334504"
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/note="clone_b
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                                                           uHisArgArgHisHisLeuHisProValSerAla***AspGlyGlnGlyProGlnThrVa
                                                                                                           TGTCCTGGGGTGGAGTGCTGCCAAGGCCATTCTGACCAGACTTTTCTGCCCCTTTGCAGGA
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REFERENCE
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Consensus quality: 243596 bases at least Q30
Consensus quality: 24396 bases at least Q30
Consensus quality: 243966 bases at least Q30
Consensus quality: 243906 bases at least Q30
Estimated insert size: 243000; agarose-fp estimation
Estimated insert size: 243000; agarose-fp estimation
Quality coverage: 7.76 in Q20 bases; agarose-fp estimation
Quality coverage: 7.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 16 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
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Center clone name: RPCI-23_85K13
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DOB Joint Genome Institute.
Sequencing of Mouse
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DOE Joint Genome Institute.
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HTG; HTGS_PHASE2; HTGS_DRAFT.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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             the accession number will be preserved.

1 18947: contig of 18947 bp in length
19048 20569: contig of 1522 bp in length
20570 20669: gap of unknown length
20570 27716: contig of 7047 bp in length
27717- 27816: gap of unknown length
27717- 27816: gap of unknown length
27718- 29329: contig of 1513 bp in length
29330 29429: gap of unknown length
29430 62474: contig of 33045 bp in length
62475 66039: contig of 3465 bp in length
62475 66039: contig of 3465 bp in length
66140 91238: gap of unknown length
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                                                                                                                                              yGlyGluLeuPheAspPheLeuAlaGluLysAsp-His***GlnArgMetArgProArgS 191
                                                                                                                                                                                                                                                                                                                                                                                                    uTyrAlaAlaLysPheIleLysLysArgArgLeuProSerSerArgArgGlyValSerAr 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCCCTGCAGTGGCCAATTTGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACGGGCATGGA 154578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            eProHisSerGly---PheAlaTleValArgLySCys-----LysGlyThrGlyMetGl
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ***LeuPheLeuGlyProArgCysArgAlaSerValLeuSerLeuLysAlaIleProLys
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                                         GTTCCTCAAACAAATCCTAGACGGTGTCCACTACCTGCACTCCAAGCGCATCGCACACTT
                                                               erSerSerSerArgSerTrpThrValSerThrThrCysThrProSerAlaSerArgThrL 211
                                                                                                                                                                                                         ACTGCATGACGTGTTCGAGAACAAGACAGATGTGGTGCTGATCCTGGAGCTGGTGTCCGG
                                                                                                                                                                                                                                  rLeuHisAspValPheGluAsnLysThrAspValValLeuIleLeuGluLeuValSerGl
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/clone_lib="RPCI mouse BAC library 23"
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-85Kl3"
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187392: gap of u
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193155: gap of u
205418: contig
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193055: contig of 4235 bp in length
193155: gap of unknown length
205418: contig of 1263 bp in length
205518: gap of unknown length
247196: contig of 41678 bp in length
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TGACCTGAAGGTGGCGCACGTTTGTGTGCGTGGGCGCGCGGGGAGGGCGGGGCAGGGGTA
                                                                                                                                                                                            LysHisTrpGly***GluMetSerLeuGlyThrLeuAspMetProGlyProHis 356
                                                                                                                                                                                                                        AlaGlyThrSerAlaAsnCys---
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                                               GI:38304023
               (Norway
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Strausberg, R. L., Feingold, E. A., Grouse, L. H., Derge, J. G., Klausner, R. D., Collins, F. S., Wagner, L., Shenmen, C. M., Schuler, G. D., Altschul, S. F., Zeeberg, B., Buetow, K. H., Schaefer, C. F., Bhat, N. K., Hopkins, R. F., Jordan, H., Moore, T., Max, S. I., Wang, J., Hsieh, F., Diatchenko, L., Warusina, K., Farmer, A. A., Rubin, G. M., Hong, L., Stapleton, M., Soares, M. B., Bonaldo, M. F., Casavant, T. L., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Scheetz, T. E., Brownstein, M. J., Usdin, T. B., Toshiyuki, S., Abramson, R. D., Mullahy, S. J., Bosak, S. A., McEwan, P. J., McKernan, K. J., Malek, J. A., Gunaratne, P. H., Richards, S., McKernan, K. J., Malek, J. A., Gayria, A. M., Gay, L. J., Hulyk, S. W., Willalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Villalon, D. K., Muzny, D. M., Sodergren, E. J., Lu, X., Gibbs, R. A., Villalon, D. K., Mitling, M., Madan, A., Young, A. C., Shevchenko, Y., Baufsard, G. G., Blakesley, R. W., Touchman, J. W., Green, E. D., Dickson, M. C., Rodriguez, A. C., Grimwood, J., Schmatz, J., Myers, R. M., Scherch, A., Schein, J. E., Jones, S. J. and Marra, M. A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

B. L. Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 137 Row: h Column: 12
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 11968141.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web Site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Blakesley,R.W., Caranite,S., Guan,X., Gupta,J., Haghighi,P.,
Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Voung & Zhang,L.-H. and Green R.
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC), Gaithersburg, Maryland;
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Direct Submission
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
                                                                                                                                          note="Vector:
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Rodentia;
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                                                                                         aSerArgThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGlnSerSe
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                               rSerValArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyLe 276
                                                                                                                                       AACATCATGTTGCTGGACAAGCATGCAGCCAGCCCACGCATTAAGCTCATCGACTTTGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="S_TKC; Region: Serine/Threonine protein kinases, catalytic domain. Phosphotransferases of the serine or threonine specific kinase subfamily. The enzymatic activity of these protein kinases is controlled by phosphorylation of specific residues in the activation segment of the catalytic domain, sometimes combined with reversible conformational changes in the C-terminal autoregulatory tail".
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GETKQETLINISAVNYDFDEEVFSSTSBLAKDFIRRLLVKDPKRRMTIAQSLEHSWIK
VRRREDGARKPERRALRAARLREYSLKSHSSWPRNTSYASFERFSRVLEDVAAAEQGL
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EARAALLGAGGLKRRLCRLENRYDALAAQVAAEVQFVRDLVRALEQERLQAECGVR"
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Conservative:
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ORIGIN		CDS	gene		source	FEATURES	TITLE JOURNAL	REMARK REFERENCE AUTHORS	TITLE	JOURNAL REFERENCE	TITLE	REFERENCE AUTHORS	SOURCE ORGANISM	ACCESSION VERSION KEYWORDS	RESULT 6 RNO6971 LOCUS DEFINITION	Db 7	5 AO		<i>t</i> .3	9 40	o o		
i	/gene="qik" /codon_start=1 /codon_start=1 /product="DAP-like kinase" /protein_id="CAA07360.1" /protein_id="CAA07360.1" /brotein_id="CAA07360.1" /db_xref="qol:038764" /db_xref="gol:038764" /db_xref="gol:038764" /db_xref="gol:038764" /translation="MSTERQBUEDHYEMGEELGSGQFAIVRKCQQKGTGMEYAAKFI /kransslation="MSTERQBUEDHYEMMITTLHDVFENKTDVVLILELVSGGELF /kransslation="MSTERQBUEDHYEMMITTLHDVFENKTDVVLILELVSGGELF /kranssrcvSredlekQildGvHYLHSKRIAHPDLkPENIMLLDKHAASFRIKLI DFGIAHRIEAGSEFKNIFGTDEFVADEINVEPLGLEADMWSIGVITYILLSGASFFI GETXQBTLTNISANNYDFDEEYFSSTSELAKDFIRRLUVXDFERRMTIAQSLEHSWIK VRREDGARKGERRURAARUREYSLKSHSGNFRNTGYASFERFSRVLEDVAAAEQGL RELQRGRRQCRERVCALRVAAEQREAGCRDGLGDLRLLRTELGRTEALRTRAQE EARAALIGAGGIKRUCALBKNYDALAAQVAAEVQFVRDUVAALEGGELQAEGCVR"	/ yetic="ctx" 114 1460	antigen" 1.1514	/mol_type="mkww" /db xref="taxon:10116" /cell_line="SV52" /cell_type="rat fibroblasts transformed with SV40 large T		4, 53117 Bonn, GERMANY lifiers	ubmission d (22-JUN-1998) Kogel D.,		Direct Submission  Direct Submission  Submitted (15-JUN-1998) Kogel D., Universitat Bonn, Institut fur  Genetik, Romerstr. 164, 53117 Bonn, GERMANY	Oncogene 20, 2645-2654 (1998) 2 XOZO1 D	Cloning and characterisation of Dlk, a novel serine/threonine kinase that is tightly associated with chromatin and phosphorylates core histones	1 Kogel,D., Plottner,O., Landsberg,G., Christian,S. and Scheidtmann.K.	rvegicus (No rvegicus ; Metazoa; ( Eutheria; F	AJ006971 AJ006971.1 GI:3250894 DAP-like kinase; dlk gene.	RNO6971 1514 bp mRNA linear ROD 16-DEC-1998 Rattus norvegicus mRNA for DAP-like kinase.		336 laAsnCysLysHisTrpGly***GluMet 345	44	16 spGlyGlnGlyProGl	Security Set   S	00	1 7	

ORIGIN

Score:

and Akira, S. which mediates Muridae; Murinae;

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RESULT 7
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VERSION
KEYWORDS
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ORGANISM
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Pred. No.:
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AB007143

Mus musculus mRNA for ZIP-kinase, c
AB007143.1 GI:2911153
ZIP-kinase.

Mus musculus (house mouse)

Mus musculus Eukaryota; Metazoa; Chordata; Crani
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Direct Submission
Submitted (10-SEP-1997) Shizuo Akira, Hyogo College of Medicine,
Department of Biochemistry; Mukogawa-cho 1-1, Nishinomiya, Hyogo
663, Japan (E-mail:akira@hyo-med.ac.jp, Tel:+81-798-45-6357,
Fax:+81-798-46-3164)
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 gThrSerCysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuAl
                                                                                     rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgAr
                                                                                                                           PheLeuAlaGluLysAsp-His***GlnArgMetArgProArgSerSerSerSerSerArgSe
                                                                                                                                                                                             GAGAACAAGACAGATGTGGTGCTGATCCTGGAGCTGGTGTCCGGTGGCGAGCTTTTCGAC
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      IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg

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Akira,S. and Kawai,T.
DNA coding for serine/threonine kinase
Patent: US 5958748-A 4 28-SEP-1999;
Location/Qualifiers
1. .1429
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                                                                                                                      GAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCATAACACTGCATGACGTGTTC
                                                                                                                                           GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
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rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgAr
                       PheLeuAlaGluLysAsp-His***GlnArgMetArgProArgSerSerSerSerSerArgSe
                                                                        GAGAACAAGACAGATGTGGTGATCCTGGAGCTGGTGTCCGGTGGCGAGCTTTTCGAC
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RESULT 9
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Sequence 4 :
AR124103
AR124103.1
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DNA coding for serine/threonine kinase
Patent: US 6171841-A 4 09-JAN-2001;
Location/Qualifiers
1. 1429
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               GluAsnLysThrAspValValLeu1leLeuGluLeuValSerGlyGlyGluLeuPheAsp 176
                                                       GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe 156
                                                                                     ATCAAGAAGCGGCGCCTGCCATCCAGCCGGCGCGCGTGTGAGCCGGGAGGAGATCGAACGC
                                                                                                  IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg 136
                                                                                                                                           PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe 116
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                                          GAGGTGAGCATCCTGCGGGAGATCCGCCAACCATCATAACACTGCATGACGTGTTC
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/mol_type="unassigned
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Gaps:
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DEFINITION
ACCESSION
Percent Similarity:
Best Local Similarity:
Query Match:
                                                        Score:
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Patent: JP 199098984-A 2 13-APR-1999;
SCIENCE & TECH AGENCY
OS Unidentified
PN JP 199098984-A/2
PD 13-APR-1999
PF 26-SEP-1997 JP 1997261589
PF 26-SEP-1997 JP 1997261589
PR SHIZUO SHINRA, TARO KAWAI
PC C12N15/09,C12N1/21,C12N9/12//(C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/C12N15/
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E23385.1 GI:
JP 1999098984
unidentified
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C12N15/09, C12N1/21, C12N9/12//(C12N15/09, C12R1:91), (C12N1/21,
C12R1:19),
C12R1:19), C12R1:19), C12N15/00, (C12N15/00, C12R1:91) CC
                                                                                                                                                                                                                             10. .13
Location/Qualifiers
                                                                                                                                                  /organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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                                                                          # synthetic construct artificial sequences.

1 (bases 1 to 185)

Park, J., Rolfs, A., Hu, Y., Shen, B.

Relley, T., Zuo, D., Raphael, J., B.

LaBaer, J. and Brizuela, L.

Cloning of human full-length CDS
recombinational vector system
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(DAPK3) mRNA, partial cds.
AY335738
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Park, J., Rolfs, A., H
Kelley, T., Zuo, D., R
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synthetic construct
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      Hu, Y., Shen, Raphael, J.,
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ui, M., Jepson, D.,
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This CDS clone is a part of a collection of human full-length expression clones generated by Harvard Institute of Proteomics. Each CDS has been cloned without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion(TM) cloning system between the Sall and HindIII sites of the pDNR-Dual vector. Additional sequences in the clone: 'ACC' after Sall site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain sequence; 'GG' after last codon and before HindIII site to maintain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-JUL-2003) Biological Chemistry and Molecular Pharmacology, Harvard Institute of Proteomics, 320 Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LaBaer, J. and Brizuela, L. Direct Submission
PheLeuAlaGluLysAspHis***-GlnArgMetArgProArgSerSerSerSerSerArgSe 196
                                                                                        GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp
                                                                                                                                    GAGGTGAACATCCTGCGGGAGATCCGGCACCCCAACATCATCACCCTGCACGACATCTTC
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kkrrllssrrgvsree erevuilreirhiitindifenkhyvliilelvsggelf
dflaekesltedeatopikqildgvhylhskriahfdlkebimklldkyvdnerkli
dfgiahkieagomefknifgtpefvapeivnyeplgleadmwsigvityillsgaspfl
getkqetlinisavnvppdeevsntsllakdpirkluvkpkrmyiiqgslehswik
airrenvrgedsgrkeerrikttrikleytikshslepnnyxadferrskvleeaaa
aebgirrelgrsrrlchedvealaaiyeekeawyreesdslgqdlrrirgellkttealk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/trans1_table=11
/product="death-associated protein kinase
/protein_id="AAQ02555.1"
/db_xref="GI.33304115"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Mutations: Stop->Leu"
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/clone_Tib="first strand cDNA from placenta and
/lab_host="pH5alpha T1 resistant"
/note="Yector: pDNR-Dual"
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|db_xref="taxon:32630"
|clone="FLH000096.01L"
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Homo sapiens mRNA for ZIP kinase,
AB022341
AB022341.1 GI:5162883
                                                                                                                                                                                          2 (bases 1 to 2055)
Iwasaki,T., Murata-Hori,M. and Hosoya,H.
Direct Submission
Submitted (12-JAN-1999) Hiroshi Hosoya, Faculty of
Science,Hiroshima University, Department of Biological Science;
Kaganiyama 1-3-1, Higashi-Hiroshima, Hiroshima 739-8526, Japan
(E-mail:hhosoya@sci.hiroshima-u.ac.jp, Tel:81-824-24-7443,
                                                                                                                                                                                                                                                                                                                                                                             kinase in HeLa cells
FEBS Lett. 451 (1), 81-84 (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                         Location/Qualifiers
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                                          cDNA library"
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   GGCCTGGAGGCGGACATGGGAGCATCGGTGTCATCACCTATATCCT---
                      rpLeuGlySer***TyrValGluHisArgArgHisHisLeuHisProValSerAla***A
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|gene="ZIPK"
|codon_start=1
|product="ZIP kinase"
|protein_id="BAA81746.1"
|db_xref="GI:5162884"
|/db_xref="GI:5162884"
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airranvrgedsgrkeerrriktytikstiskslepnovaadferesvlleaaa
aeeglrelgrsrrlchedvealaaiyeekeamyreesdslgodlrelrgellktealk
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JOURNAL
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                                                                                                                                                                                                                                                                 No.:
                                                                                                                                                                                                     Match:
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Patent: JP 2002017375-A 2718 22-JAN-2002;

HELIX RESEARCH INSTITUTE

SS Homo sapiens (human)
PN JP 2002017375-A/2718
PD 22-JAN-2002
PD 22-JAN-2002
PD 22-JAN-2002
PI TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
PI ISHII,
PI TURIK KAWAI,AI WAKAMATSU,TOMOYASU SUGIYAMA,KEIICHI NAGAI, PI
SHINICHI KOJIMA,
PI TETSUJI OTSUKI,HISASHI KOGA
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PC
                                                                                                                                                        (1-361) x BD127287 (1-2079)
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Mammalia; Eutheria, Primates; Catarrhini; Hominidae; Ho
1 (bases 1 to 2079)
Ota,T., Nishikawa,T., Isogai,T., Hayashi,K., Ishii,S.,
Wakamatsu,A., Sugiyama,T., Nagai,K., Kojima,S., Otsuki,
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                                ATCAAGAAGCGCCGCCTGTCATCCAGCCGGCGTGGGGTGAGCCGGGAGGAGGATCGAGCGG
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                                                                                           TTTGCGATCGTGCGGAAGTGCCGGCAGAAGGGCACGGCAAGGAGTACGCAAGTTC
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mer for synthesizing full-length cDNA and use thereof FH I
Location/Qualifiers
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TOSHIO OTA,TETSUO NISHIKAWA,TAKAO ISOGAI,KOJI HAYASHI,SHIZUKO
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                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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2 (bases 1 to 2079)
Isogai,T. and Otsuki,T.
Direct Submission
Submitted (25-MAR-2002) Takao Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
                                                                                                              Isogai,T., Ota,T., Nishikawa,T., Hayashi,K., Otsuki,T., Suguiyama,T., Suzuki,Y., Nagai,K., Sugano,S., Ishii,S., Kawai-Hio,Y., Saito,K., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Kojima,S., Nagahari,K., Masuho,Y., Ono,T., Okano,K., Yoshikawa,Y., Aotsuka,S., Sasaki,N., Hattori,A., Okumura,K., Iwayanagi,T. and Ninomiya,K.
                                                                                                                                                                                                                                                                     AK074799.1 GI:22760480 oligo capping; fis (full insert sequence). Homo sapiens (human)
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AK074799
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CCCAGAGATTGTGAACTATGAGCCGCTG 651

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0у 1	Qy 1 Db 1	Qy Db 1	FIGURE9 (1-	Alignment Scores: Pred. No.: Score: Percent Similarity Best Local Similar: Query Match: DB:	FEATURES SOUICE	COMMENT
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	Oy 157 GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp 176	* · · · · ·
<u>, , , i.a.</u>	Qy 137 GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe 156	<b>.</b> .
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	Qy 99 PheAlaIleValArgLysCysLysGlyThrGlyMetGluTyrAlaAlaLysPhe 116	
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E 1 (Dases 1 to 666)

NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
cDNA Library Preparation:
cDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be info@mage.llnl.gov BU670814 666 bp mRNA linear EST 01-NISC 1r01e11.y1 NCI CGAP Pr49 Rattus norvegicus cDNA clone IMAGE:5598044 5', mRNA sequence. Rattus norvegicus (Norway rat) Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; BU670814 GI:23398790 EST. Rattus. EST 01-OCT-2002

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CA334157 637 bp ml
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IMAGE:5599435 5', mRNA sequence.
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/lab_host="DH10B (T1 phage-resistant)"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NCI_CGAP_Pr49"
/clone_rib="NCI_CGAP_Pr49"
/note="NCIgan: prostate; Vector: pCMV-SPORT6.1; Site_1:
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/note-"Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
/note-"Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
/note-"Organ: prostate from 11 wk male, 3 days
/nost-castration, average insert size 2 kb), NCI_CGAP_Pr40
/richial prostate from 11 wk male, 7 days
/richial prostate from 11 wk male, 7 days
/richial prostate from 11 wk male, 7 days
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/richial prostate from 12 wk male,
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/clone="IMAGE:5598044"
/sex="male"
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15 norvegicus cDNA clone
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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EST.
Rattus norvegicus (Norway rat)
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Unpublished (1997)
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National Cancer Institute, Cancer Genome Anat
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                                                                                         ACTITICGACTITCTGGCTGAGAAGGA-TCACTGACAGAGGATGAGGCCACGCAGTTCCT
                                                                                                                                                                                                                                                                                          GATCGAGCGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCATCACGCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                  GGCCAAGTTCATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGCGGTGTGAGCCGTGAGGA
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                                    ACTITICGACTITCIGGCIGAGAAGGAGTCACIGACAGAGGATGAGGCCACGCAGTICCT
                                                                                                                                                                                                                        CGATGTGTTCGAGAACAAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGCGA
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//dev stage="adult, 11 week"
//lab host="phil08 (T1 phage-resistant)"
//clone_lib="NCI_CGAP_Pr50"
//note="Crgan: prostate; Vector: pcWV-SpORT6.1; Site 1:
//note="Crgan: prostate; Vector: pcWV-SpORT6.1; Site 1:
//note="Crgan: prostate; Vector: pcWV-SpORT6.1; Site 1:
//note="Crgan: prostate; Vector: pcWV-SpORT6.1; Site 1:
//note="Crgan: prostate; Vector: pcWV-SpORT6.1; Site 1:
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//note="Crgan: pcWV-SpORT6.1; Site 1:
//note="Crgan: pcWV-SpORT6.1; Site 1:
//note="Crgan: pcWV-SpORT6.1; Si
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/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="IMAGE:5599435"
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Pred. No. 3.2e-158;
0; Mismatches 0;
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Length 637; Indels

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Gaps

347

233

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353

293

413

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SOURCE
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AUTHORS
TITLE
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                                                                     Query Match 24.4%; Sometime Best Local Similarity 100.0%; I Matches 267; Conservative 0;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL

CDNA Sequencing by: National Institutes of Health Intramural

Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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Unpublished (1997)
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NISC 1r05b04.y1 NCI CGAP Pr49 Rattus
IMAGE:5598270 5', mRNA sequence.
BU671103
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National Cancer Institute, Cancer Genome Anatomy
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CAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGC
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                                                                                                                                                                                     /dev stage="adult, 11 week"

//ab host="DHHOB (T] phage-resistant)"

//clome_lib="NCI_CGAP_Pr49"

//note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
//note="Organ: prostate from 11 wk male, 3 days
//nost-castration, average insert size 2 kb), NCI_CGAP_Pr40
//organ: prostate from 11 wk male, 5 days
//organ: prostate from 11 wk male, 7 days
//organ: pr41 (ventral prostate from 11 wk male, 7 days
//organ: pr41 (ventral prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
//organ: prostate from 11 wk male, 7 days
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//organ: prostate from 11 wk male, 7 days
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/mol_type="mRNA"
/db xref="taxon:10116"
/clone="IMAGE:5598270"
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                                                                     Score 267; DB; Pred. No. 1.3
                                                                     ; DB 13; I
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       285
                                                 829
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110 CAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGC 169
                                                                                                                                                                                                                                                                                                                                                         267;
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Rattus norvegious
Eukaryota; Metazoa; Chordata;
Eukaryota; Metazoa; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CB766821 417 bp mRNA
AMGNNUC:SRDB2-00314-C4-A srpb2 (10220) I
srpb2-00314-c4 5', mENA sequence.
CB766821 GB:29855212
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Amgen Rat EST Program
Unpublished (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dan Fitzpatrick
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plate: 00314 row: c
                                                                                                                                                                                                                                                                                                                                                                               h 19.9%;
Similarity 99.6%;
                        CTTGGCCTGACCTGCCTCAACAATCCTGTCTTCCACAGCCCCTGAGATTGTAAACTATGA 888
                                                                                                                            CAGAGTTCGTCGGTGAGGGGCAGGTGTGGGCACCACCCGATAGGGTAGATTTTGCACGGC 828
                                                                                                                                                                            ACTTTGGCATCGCGCACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCACGC 224
                                                                                                                                                                                                                ACTTTGGCATCGCGCACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCACGC
                                                                                                                                                                                                                                                                   ACTITICGACTITICIGGCTGAGAAGGA 554
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                                                                                    CAGAGTTCGTCGGTGAGGGGCAGGTGTGGGCACCACCCGATAGGGTAGATTCTGCACGGC
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                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="prostate tissue"
/clone_lib="srpb2 (10220)"
/note="Vector: pspORT1; Site_1: Sall; Site_2:
prostate normalized double selected poly(A+) m
fraction > 1 kb"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="srpb2_00314-c4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                       Score 217; DB 14;
Pred. No. 6.5e-96;
0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 417;
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REFERENCE
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MEDLINE
PUBMED
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Coordinated Laboratory for Computational Genomics University of Iowa 375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BF547702

UI-R-AO-bf-a-02-0-UI.rl UI-R-AO Rattus norvegicus cDNA clone
UI-R-AO-bf-a-02-0-UI.r. MRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bento-soares@uiowa.edu
CDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.
This clone is also available through the I.M.A.G.E. Consortium
LLNL (info@image.llnl.gov). IMAGE ID= 1769507
Seq primer: M13 Forward.
Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genome Res. 6 (9), 791-806 (1996) 97044477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Rodentia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BF547702
BF547702.1 GI:11638809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Soares, MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  discovery
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ACAAGACAGAIGTGGTGCTGAICTTGGAGCTGGTGTCCGGCGGCGAACTTTTCGACTTTC
                                                                                                                                                           AGAAGCGGCGCCTGCCGTCCAGCCGGCGCGCGGTGAGCCGTGAGGAGCATCGAGCGCGAGG 421
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                                                       TGAGCATCCTGCGCGAGATCCGCCACCCCAACATCATCACGCTGCACGATGTGTTCGAGA
                                                                                     TGAGCATCCTGCGCGAGATCCGCCACCCCAACATCATCACGCTGCACGATGTGTTCGAGA
                                                                                                                        AGAAGCGGCGCCTGCCAGCCGGCGCGCGTGAGCCGTGAGGAGATCGAGCGCGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 565)
                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                               /clone lib="UI-R-AO"
/note="Vector: pT/T3D-Pac (Pharmacia) with a modified /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; This library consists of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture."
                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/db xref="taxon:10116"
/clone="UI-R-A0-bf-a-02-0-UI"
/dev_stage="adult"
/lab_host="DHIOB (Life Technologies)"
/lab_host="DHIOB (Life Technologies)"
/clone_lib="UI-R-A0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Rattus norvegicus"
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                                                                                                                                                                                                             17.7%;
100.0%;
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                                                                                                                                                                                                             Score 193; DB 10;
Pred. No. 5.4e-84;
                                                                                                                                                                                              Mismatches
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Best Local Similarity
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                                                                                                                                                         AMGNNUC:SRPB2-00315-F4-A srpb2 (10220) srpb2-00315-f4-5', mRNA sequence. CB801518 CB801518.1 GI:29914858 EST.
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AMGNNUC:NRPI4-00055-H4-A W Rat I
CDNA Clone nrpi4-00055-h4 5', mi
                                                                                                                     Rattus norvegicus (Norway rat)
Rattus norvegicus
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Amgen Rat EST Program
Unpublished (2003)
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1 (bases 1 to 412)
Amgen EST Program.
Amgen Rat EST Program
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Tel: 805 447-4881
Plate: 0055 row: h column: 4.
Location/Qualifiers
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                                                                              Mammalia; Eutheria;
                                                                                                    Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                GGCCAAGTTCATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGCGCGTGAGCCGTGAGGA 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCAAGTTCATAAAGAAGCGGCGCCTGCCGTCCAGCCGGCGCGCGTGTGAGCCGTGAGGA 407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.3%; So llarity 100.0%; I Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="nrpi4-00055-h4"
/clone lib="W Rat pituitary (10472)"
/note="Vectoor: pspORT1; Site 1: Sal1;
pituitary adult female Wistar rat avg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'mol_type="mRNA"
'db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Rattus norvegicus"
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Rodentia;
                                                                                Chordata; Craniata; Vertebrata; Euteleost
Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 178; DB 14;
Pred. No. 1.3e-76;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thousand Oaks,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             שעע mRNA linear
t pituitary (10472) RamRNA sequence.
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                                                                                                                                                                                                                                                                 mRNA
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                                                                                                                                                                                                                                                Rattus
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                                                                                                                                                                                                                                            linear EST 1
cus norvegicus
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                                                                                                      Euteleostomi;
                                                                                                                                                                                                                                                EST 16-MAY-2003
jicus cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EST 11-APR-2003
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REFERENCE
AUTHORS
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CB749794
LOCUS
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ORGANISM
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VERSION
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Matches
      Query Match
Best Local Similarity
Matches 150; Conserva
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CB749794 440 bp mRNA line
AMGNNUC:MRPE4-00018-H10-A mrpe4 (10380) Rattus
Clone mrpe4-00018-h10 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 440)
Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   One Amgen Center Drive, Thousand Oaks, Tel: 805 447-4881
Plate: 00315 row; f column: 4.
                                                                                                                                                                                                                                                                                                           Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CB749794.1 GI:29817096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2003)
Contact: Dan Fitzpatrick
Amgen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAGAGTTCGTCGGTGAGGGGCAGGTGTGGGCACCACCGATAGGGTAGATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACTTTGGCATCGCGCACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amgen Center Drive, Thousand Oaks, 805 447-4881
te: 00018 row: h column: 10.
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.6%; Solitarity 100.0%; I Conservative 0;
                                                                                 /tissue_type="placenta embryo"
/clone_Tib="mrpe4 (10380)"
/note="Vector: pspoRT1; Site_1:
placenta embryo day 17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="prostate tissue"
/clone_lib="srpb2 (10220)"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: NotI; rat
prostate normalized double selected poly(A+) mRNA size
fraction > 1 kb"
                                                                                                                                                                 /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                            018 row: h column:
Location/Qualifiers
                                                                                                                                                clone="mrpe4-00018-h10"
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/clone="srpb2-00315-f4"
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13.7%; but
100.0%; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type="mRNA"
                  Score 150; DB 14;
Pred. No. 9.6e-63;
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Pred. No. 3.8e-73;
0; Mismatches 0;
      Mismatches
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      0
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                                      440;
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CB741392
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Best Local S
Matches 251
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TITLE
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                                                                                                                                                                                                                                                                                         184 CATCCTGCGCGAGATCCGCCACCCCAACATCATCACGCTGCACGATGTGTTCGAGAACAA
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                                                                                                                                                                                                                                                                                                                                                        251;
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CB741392
CB741392.1 GI:29808681
EST.
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455 bp mRNA linear EST 11-APR-2003
AMGNNUC:NRWA3-00012-F6-A white adipose tiss (10469) Rattus
norvegicus cDNA clone nrwa3-00012-f6 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              One Amgen Center Drive, Thousand Tel: 805 447-4881 Plate: 00012 row: f column: 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                   GTTGCTGGACAA
                                                                GTTGCTGGACAA
                                                                                                  TGTCCACTACCTGCACTCCAAGCGCATCGCGCACTTTGACCTGAAGCCGGAGAACATCAT
                                                                                                                        TGTCCACTACCTGCACTCCCAAGCGCATCGCGCACTTTGACCTGAAGCCGGAGAACATCAT
                                                                                                                                                             TGAGAAGGAGTCACTGACAGAGGATGAGGCCACGCAGTTCCTCAAGCAGATCCTGGACGG
                                                                                                                                                                                            TGAGAAGGA-TCACTGACAGAGGATGAGGCCACGCAGTTCCTCAAGCAGATCCTGGACGG 604
                                                                                                                                                                                                                          GACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGAGCTTTTCGACTTTCTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="adipose tiss"
/clone_Tib="white adipose tiss (10469)"
/note="Vector: pSpCRT1, Site_1: Sal1; Site_adipose tiss adult female Wistar rats, >250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Rattus norvegicus"
/mol type="mRNA"
/db xref="taxon:10116"
/clone="nrwa3~00012-f6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               012 row: f column:
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  12.0%;
                                   435
                                                                  676
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Pred. No. 2.5e-53;
0; Mismatches 0;
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Length Indels

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REFERENCE
AUTHORS
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CB803207
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AUTHORS
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BG663786
LOCUS
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Best Local
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                                                                                   TITLE
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Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB803207 410 bp mRNA linear EST 16-MAY-2003
AMGNNUC:MRPE3-00033-D9-A placenta embryo D17 (10379) Rattus
norvegicus cDNA clone mrpe3-00033-d9 5', mRNA sequence.
                                                 1 (bases 1 to 411)
Xiao, H.S., Huang, O.H., Zhang, F.X., Bao, L., Lu, Y.J., Guo, C., Yang, L., Huang, W.J., Fu, G., Xu, S.H., Cheng, X.P., Yan, Q., Zhu, Z.D., Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.
Zhang, X., Chen, Z., Han, Z.G. and Zhang, X.
Identification of gene expression profile of dorsal root ganglion in the rat peripheral axotomy model of neuropathic pain proc. Natl. Acad. Sci. U.S.A. 99 (12), 8360-8366 (2002)
                                                                                                                                                                                                                                                                                          BG663786
DRAAANF02 Rat DRG Library
5', mRNA sequence.
BG663786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 One Amgen Center Drive, Thousand Oaks, Tel: 805 447-4881
Plate: 00033 row: d column: 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus
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                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                          Rattus norvegicus
                                                                                                                                                                                                                                                                             BG663786.1 GI:13885708
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                                                                                                                                                                       Rattus.
                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
Contact: Zhang Xu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCACCCCAACATCATCACGCTGCACGATGTGTTCGAGAACAAGACAGATGTGGTGCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  CTTGGA 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTGGA 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCACCCCAACATCATCACGCTGCACGATGTGTTCGAGAACAAGACAGATGTGGTGCTGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="mrpe3-00033-d9"
/tlssue type="placenta embryo"
/clone Iib="placenta embryo D17 (10379)"
/note="Vector: pSPORT1; placenta embryo D17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 126; DB 14; Pred. No. 7.1e-51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                            7 Rattus norvegicus
                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CA 91320-1799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 410;
                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                            linear EST 30-APR-2001
cDNA clone DRAAANF02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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JOURNAL COMMENT
                                                                                                                                           REFERENCE
AUTHORS
TITLE
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SOURCE
                                                                                                                                                                                                                                                                                                         ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 12
CB787038
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               FEATURES
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Best Local Similarity
                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: xu.zhang@ion.ac.cn
This clone is also available at Chinese National Human Genome
This clone is also available at Chinese National Human Genome
Center at Shanghai, 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park,
Pudong New Area, P.R.China. Please contact with Zhang Xu
(xu.zhang@ion.ac.cn) or Han Zeguang (hanzg@chgc.sh.cn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Laboratory of Sensory System
Institute of Neuroscience
320 Yue Yang Road, Shanghai 200031, P.R.China
Tel: 86-21-64748700-121
                                                                                                                                                                                                                  Rattus norvegicus
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                            CB787038 451 bp
AMGNNUC:MRBE3-00123-E9-A rat brain
CDNA clone mrbe3-00123-e9 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: T3 POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FORWARD: T3
BACKWARD: T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 86-21-64713446
                                                                                                                           Amgen EST Program.
Amgen Rat EST Program
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                              CB787038
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One Amgen Center Drive, Thous:
Tel: 805 447-4881
Plate: 00123 row: e column:
Location/Qualifiers
1. .451
                                                                                                                                                                                                   Rattus.
                                                                                                                                                                                                                                                                      Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                             CB787038.1 GI:29875429
                                                                                                        Contact: Dan Fitzpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGTAGCGAGTTCAAGAACATCTTTGGCACGCCAGAGTTCGTCG 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACATGCAGCCAGCCCACGCATTAAGCTCATCGACTTTGGCATCGTGCACAGGATCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGCATGCAGCCAGCCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAGG 735
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCGGTAGCGAGTTCAAGAACATCTTTGGCACGCCAGAGTTCGTCG
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                                                                                      Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol type="mRNA"
/strain="Sprague-Dawley"
/db xref="taxon:10116"
/clone="DRAAANF02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="dorsal root ganglion"
/dev_stage="adult"
/clone_lib="Rat DRG Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.3%;
                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 123; DB 12;
Pred. No. 2.2e-49;
0; Mismatches 2;
                                                                       Thousand
                                                                         Oaks,
                                                                                                                                                                                                                                                                                                                                              mRNA linear EST 16-MAY-2003
E15 (10374) Rattus norvegicus
sequence.
                                                                         CA 91320-1799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 225
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REFERENCE
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AA966990
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KEYWORDS
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JOURNAL
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 136)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

The WashU-HMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      μα38h03.rl Scares mammary gland NbMMG Mus musculus cDNA clone IMAGE:1349045 5' Similar to SN:DAPK HUMAN P53355 DEATH-ASSOCIATED PROTEIN KINASE 1 ;, mRNA sequence.

AA966990
                                                                                                                                                                                                                                                                                                                                                         Possible reversed clone: similarity on warseq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:697837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA966990.1 GI:3140883
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAGCGGCCAGTTCGCCATCGTGCGCAAGTGCCAGCAGAAGGGCACCGGCATGGAGTACGC
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                                                                                                                                                                                                                                                                                                                                                                                                                               considered overall poor quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="brain E15"
/clone_libs"rat brain E15 (10374)"
/note="Vector: pBCB; Site_1: BstXI; Site_2: Not1; rat brain E15"
/clone_lib="Soares_mammary_gland_NbMMG"
/note="Organ: mammary_gland; Vector: pT7T3D-Pac
/note="Organ: mammary_gland; Vector: pT7T3D-Pac
/pharmacia) with a modified polylinker; Site 1:
Site_2: Eco RI; 1st strand cDNA was primed with
                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                               /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                       /sex="male"
                                                                                                                                                                                           /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:1349045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="mrbe3-00123-e9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                     organism="Mus musculus"
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Pred. No. 1.8e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 451;
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                              Not
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ACCESSION
VERSION
KEYWORDS
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AA027503
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Best Local S
Matches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 216)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dul
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA027503 216 bp mRNA linear EST 21-JAN mi04e11.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus clone IMAGB:459500 5' similar to PIR:S39269 S39269 DAP-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 205. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This clone is available royalty-free through LLNL; IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human ;, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mouseest@watson.wustl.edu
                 /clone lib="Soares mouse placenta 4NbMP13.5 14.5"

/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)

with a modified polylinker; site 1: Not I; Site 2: Eco

1st strand cDNA was primed with a Not I - oligo(dT) pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. Library constructed and normalized by Bento Soares and M.Fatima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oligo(dT) primer
went through one round of normalization,
                                                                                                                                                                                                       /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                   sex="unknown"
                                                                                                                                                                                                                                                                                              clone="IMAGE:459500"
                                                                                                                                                                                                                                                                                                                db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                 mol_type="mRNA"
strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
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REFERENCE
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JOURNAL
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Best Local Similarity
Matches 44; Conserv
                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 235)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
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n quality sequence stop: 205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            314 286 1800
314 286 1810
4.0%; Score 44; DB 9; Let ilarity 100.0%; Pred. No. 2.3e-10; Conservative 0; Mismatches 0;
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                                                                                   /clone lib="Soares mouse placenta 4NDMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco
1st strand cDNA was primed with a Not I - oligo(dT) pr
                                                                                                                                                                                                                                                                                                  /tissue_type="placenta"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
                                                                                                                                                                                                                                                                                                                                            sex="unknown"
                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
/clone="IMAGE:459664"
                                                                                                                                                                                                                                                                                     lab_host="DH10B"
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100.0%;
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Pred. No.
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O. 2.3e-10;
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                                  Length 235;
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AA864020
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                                                                                                         Query Match
Best Local
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murina
1 (bases 1 to 316)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dub
Marra, M., Hillier, L., Allen, M., Le, M., Martin, J., Morris, M.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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vx88a02.rl Soares thymus 2MbMT Mus musculus cDNA clone
IMAGE:1282250 5' similar to SW: DAPK_HUMAN P53355 DEATH-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trace considered overall poor quality possible reversed clone; similarity on wrong strand Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1996)
Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Lo
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                                                                                                           Similarity
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                                        CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 228
                                                                                      Conservative Conservative
                                                                                                                                                                                                                  rounds of normalization, and v
Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Thymus"
/dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone="IMAGE:1282250"
                                                                                      0;
                                                                                                           Score 44;
Pred. No.
                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                           DB 9; Le
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Louis,
                                                                                                                              Length 316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dietrich, N., Dubuque, T
                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contact the
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                                                                                           0
                                                                                           Gaps
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ACCESSION
VERSION
KEYWORDS
                                                                               RESULT 18
AA013814
LOCUS
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AA027379
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ORGANISM
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                                                             DEFINITION
                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                 415
                                                                                                                                                                                                                                                      44;
                    AA013814 340 bp mh06f01.r1 Scares mouse placenta clone IMAGE:441721 5' similar to human ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu, Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Mozris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA027379

331 bp mRNA linear EST 21-JAN-1997
mi05c03.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA
clone IMAGE:459556 5' similar to PIR:S39269 S39269 DAP-kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA027379.1 GI:1493509
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AA027379
    AA013814
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                                                                                                                                                                             CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 331)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 315.
Location/Qualifiers
                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                             T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT/T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-Pac (pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:459556"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sex="unknown"
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                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                            4.0%;
                                                                                                                                                                                                                                                  ; Score 44; DB
%; Pred. No. 2.6
0; Mismatches
                                                                                                                                                                                                                                                                      DB 9; L, 2.6e-10;
                                      mRNA linear EST 21-JAN-19:
4NbMP13.5 14.5 Mus musculus cDNA
PIR:S39269 S39269 DAP-kinase -
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                                                                                                                                                                                                                                                                                      Length 331;
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REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                         RESULT 19
BE654598
LOCUS
DEFINITION
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ORGANISM
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AUTHORS
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                                                                                                                                      KEYWORDS
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Best Local Similarity
Matches 44; Conserv
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8
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Fax: 314 286 1810
                                                                                                                                                        BE654598.1
                                                                                                                 Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
1 (bases 1 to 340)
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EST.
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ilarity 100.0%;
Conservative (
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sex="unknown
                                                                                                                                                        GI:9980511
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693 CGCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAGGC 736
Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Eukaryota; Metheria; Rodentia; Sciurogna Mammalia; Eutheria; Rodentia; Sciurogna 1 (bases 1 to 343)

Bonaldo, M.F., Lennon, G. and Soares, M.B. Normalization and subtraction: two appr
                                                                                                                                                                                                                                         BE654598 arNA linear UI-M-AJI-agz-e-10-0-UI.rl NIH BMAP MOB N Mus muscu UI-M-AJI-agz-e-10-0-UI 5', mRNA sequence.
BE654598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
This clone is available royalty-free tl
IMAGE Consortium (info@image.llnl.gov)
MGI:267057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (1996)
Contact: Warra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Ld
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Du
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
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The WashU-HHMI Mouse EST Project
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T 3'1; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
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/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: Not I; Site_2: Eco
ist strand cDNA was primed with a Not I - oligo(dT) pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
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/clone="IMAGE:441721"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44; DB; Pred. No. 2.6
                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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3. 2.6e-10;
0;
  two approaches
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v) for further ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 340;
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ORGANISM
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                                                                                                                                                                                                               1 (bases 1 to 354)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
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CDNA Library Preparation: M.B. Soares Lab Clone distribution:

Researchers may obtain BMAP cDNA clones from RESEARCH GENETICS. It

should be noted that Bento Soares is generating a small number of

additional specialized non-redundant arrays of EMAP cDNAs whose

availability will be considered under appropriate and limited
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA982305 354 bp mRNA linear EST 27-MAY-19 ua53b01.rl Soares thymus 2NbMT Mus musculus cDNA clone IMAGE: 361161 5' similar to SW:DAPK_HUMAN P53355 DEATH-ASSOCIATED
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Tel: 301 443 1706
Fax: 301 443 9890
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97044477
                               WashU-HHMI Mouse EST Project
Washington University School of MedicineP
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            collaborative arrangements
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6001 Executive Blvd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Chin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8889548
                                                                                                               Contact: Marra M/Mouse EST Project
                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                   The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA982305.1 GI:3160964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEIN KINASE 1 ;, mRNA sequence.
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 musculus (house mouse)
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/clone lib="NIH_BMAP NOB N"
/clone lib="NIH_BMAP NOB N"
/clone lib="NIH_BMAP NOB N"
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/note="Vector: pT7735-Pac (Pharmacia) with a modified
/note="Vector: pT7735-Pac (Pharmacia) with a modified
/note="Vector: pT7735-Pac (Pharmacia) with a modified
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/note="Vector: pT7735-Pac (Pharmacia) w
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/dev_stage="27-32 days"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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100.0%; Pr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; I
. 2.6e-10;
ches 0;
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ACCESSION
VERSION
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Best Local
                                                                                                                                                                                                                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415 CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
                                                                                                                                                                                                                     1 (bases 1 to 376)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Du
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA023436 mRNA linear EST 21-JAN mh72f07.r1 Soares mouse placenta 4NbMP13.5 14.5 Mus musculus clone IMAGE:456517 5' similar to PIR:S39269 S39269 DAP-Kinase
                                                       WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                         Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further:
                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human ;, mRNA sequence.
AA023436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA023436.1 GI:1487369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6J"
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hes 0;
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                                                                                                                                                                                                                                             od, K., Moore, B., Wilson, R. and
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    information.
                   contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  musculus cDNA
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SOURCE
ORGANISM
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AA024296
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VERSION
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                      source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA024296 385 bp mRNA linear EST 21-JAN-199 mh92a05.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:458384 5' similar to PIR:S39269 S39269 DAP-kinase -
                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (Dases 1 to 385)

1 (Dases 1 to 385)

Garra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human ;, mRNA sequence.
AA024296
                                                                           MGI:275272
Trace considered overall poor quality
Possible reversed clone: similarity on
Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
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                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                          The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                  Waterston,R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     primer: -28M13 rev2 from
                                   quality sequence stop: 1.
Location/Qualifiers
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T 3']; double-stranded cDNA was ligated to Eco RI adapy (Pharmacia), digested with Not I and cloned into the NI and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone lib="Soares mouse placenta 4NbMP13.5 [4.5" /note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; ist strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2
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/clone="IMAGE:456517"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 44; DB 9; I
Pred. No. 2.7e-10;
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                                                                                                   Buoza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 376;
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                                                                                                                                                                                                                                                                        MO 63108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RI adaptors
to the Not I
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SOURCE
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W75433
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W75433 395 bp mRNA linear EST 20-JUN me50d04.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNV clone IMAGE:390919 5' similar to PIR:S39269 S39269 DAP-kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 395)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Lotel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human ;, mRNA sequence. W75433
                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W75433.1 GI:1385647
                                                                                                                                                                                                                                                                               MGI:242751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
                                                                                                                                                                                                                                                         primer: mob.REGA+ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (house mouse)
                                                                                                                                                                                                                                   quality sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1; Not I; Site 2: Eco RI;
lst strand cDNA was primed with a Not I - oligo(dT) primer
                                                                                                                 strain="C57BL/6J"
                                                                                                                                     mol_type="mRNA"
                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
clone="IMAGE:458384"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mol_type="mRNA"
|strain="C57BL/6J"
'tissue_type="embryo"
'dev_stage="13.5-14.5dpc total fetus"
                                              sex="unknown"
                                                                     clone="IMAGE:390919"
                                                                                             db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tissue_type="placenta"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.0%; Score 44;
00.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                   stop: 328.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; Le
2.7e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                          Louis, MO
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                                                                                                                                                                                                                                                                                                                                                                                                                            63108
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ORGANISM
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Best Local Similarity
                                                                                                                                                                                                                                                                                   source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 397)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptce, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                         Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human ;, mRNA sequence.
AA020495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA020495 397 bp mRNA linear EST 21-JAN-1997 mh61g04.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:455478 5' similar to PIR:S39269 S39269 DAP-kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                       MGI:272366
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
                                                                                                                                                                                                                                                                                                                                                   primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               musculus (house mouse)
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                                                                                                                                                                                                                                                                                                       quality sequence stop: 355.
Location/Qualifiers
/clone lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo dT) primer
                                                                                 /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                   /mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                 organism="Mus musculus"
                                                                                                                                                      sex="unknown"
                                                                                                                                                                                                 db_xref="taxon:10090"
                                                                                                                                                                             lone="IMAGE:455478"
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RESULT 24 AA020495 LOCUS

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ACCESSION VERSION

KEYWORDS

REFERENCE

AUTHORS

FEATURES

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AA013793
LOCUS
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AUTHORS
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VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                    source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 399)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
Contact: Marra M/Mouse EST Project
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mhl3e04.rl Soares mouse placenta 4NbMPl3.5 14.5 Mus musculus cDNA clone IMAGE:442398 5' similar to PIR:S39269 S39269 DAD NICHTELE CONA human : mpNA german
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MGI:267734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA013793.1 GI:1474859
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: ETPrimer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                      quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                /clone lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco
1st strand cDNA was primed with a Not I - oligo(dT) pr
[5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:442398"
                                                                                                                                                                                                                                                                                                                                                                                                  ity sequence stop: 342.
Location/Qualifiers
                                                                                                                                                                                                                                                                     sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 44; DB 9; Pred. No. 2.7e-1
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                                                                                                                                  Eco RI;
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JOURNAL COMMENT
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                      44;
                                                                                                                                                   405 bp mRNA linear EST 27-SE ux20d04.yl Soares thymus 2NbMT Mus musculus cDNA clone IMAGE:3472039 5' Similar to TR:054784 O54784 DEATH-ASSOCIATED KINASE 3;, mRNA sequence.
BE8537.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Abt.Lehrach
Max Planck Institut Fuer Molekulare Genetik
Ihnestrasse 73, Berlin, 14195 Germany
The cDNA libraries ICREp 522 and 523 were normalized with
oligonucleotide fingerprinting, resulting in a unique subset
5376 cDNA clones.
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Eickhoff, H., Schuchhardt, J., Ivanov, I., Meier-Ewert, S., O'Brien, J. Malik, A., Tandon, N., Wolski, E., Nyarsik, L., Bohlfs, E., Nyarsik, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genome Res. (2000) In press
Contact: MPIMG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malik,A., Tandon,N., Wolski,E., Rohlfs,E., Nyarsik,L.,
Reinhardt,R., Nietfeld,W. and Lehrach,H.
Tissue gene expression analysis using arrayed normalized cDNA
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AL363655.1
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AL363655 ICRFp
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 405)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                       Mus musculus
                                                                                                                              BE853739.1 GI:10312309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="embryo"
/dev_stage="9 and 12 pc embryo"
/clone_lib="ICRFp 522 and 523"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="K9322B48"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
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100.0%; Pr
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100.0%;
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K9322B48 5',
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E 1 (Dases 1 to 422)

S Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T., Hayatsu, N., Hiramoto, K., Hiracka, T., Hirozane, T., Imotani, K., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R., Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            415 CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
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EST.
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BB849679
   Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 348 Location/Qualifiers
                                                                                        Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
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|sex="male"
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strain="C57BL/6J"
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100.0%; Pred. No. 2.7e-1
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hes 0;
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       Kanagawa 230-0045, Japan
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URL:http://genome.gsc.riken.go.jp/

Carrinci.p., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,

Icbh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new

genes. Genome Res. 10 (10), 1617-1630 (2000)

wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,

wagi,K., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,

Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A.

and Hayashizaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44;
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Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of nonredundant cDNA library. Genome Res. . 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.

e mouse tissues.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA050632 423 bp mRNA linear EST 09-SEP-mj18e05.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:476480 5' similar to PIR:S39269 S39269 DAP-kinase -
Contact: Marra M/Mouse BST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                           1 (bases 1 to 423)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
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Mammalia; Eutheria; Rodentia;
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81-45-503-9216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
/mol_type="mRNA"
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/dev_stage="adult"
/clone_lib="RIKEN_full-length_enriched, adult_inner_ear"
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/clone="F930102A07"
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     Louis,
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JOURNAL
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 CGCGAGGTGAGCATCCTGCGCGAGATCGCCCAACATCAT 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 W85231
mf52b04.rl Soares mouse embryo Nbi
clone IMAGE:408655 5' similar to
human ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44;
                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 r (bases 1 to 423)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                             W85231.1
EST.
                                                                                      Unpublished (1996)
On Sep 12, 1996 this sequence version replaced gi:1397701.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vector to vector length is 475 Seq primer: -28M13 rev2 from Ame High quality sequence stop: 401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This clone is available royalty-free through LLNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGI:287224
                   Email: mouseest@watson.wustl.edu
This clone is available royalty-
                                                     Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                      The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
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/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'db_xref="taxon:10090"
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ailable royalty-free through LLNL; contact the (info@image.llnl.gov) for further information.
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Pred. No.
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NbME13.5 14.5 Mus musculus cDNA
to PIR:S39269 S39269 DAP-kinase
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. 2.8e-10;
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IMAGE Consortium

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Nasukawa, T., Adachi, J., Bono, H., Kondo, S.,

Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I.,

Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,

Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,

Beisel, K.W., Baldarelli, R., Hill, D.P., Bult, C.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,

Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,

Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,

Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,

Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B.L., Konagaya, A.,

Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Magjott, D.R.,

Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,

Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S.,

Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ramachandran, S.,

Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,

Verardo, R., Magner, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I.,

Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGI:252423
Seg primer: -28M13 rev2 Irum ...
High quality sequence stop: 410
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 428)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus
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44; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus"
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. 2.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murinae;
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RESULT 32
BF147326
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      ACCESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: genome-resegsc.riken.go.jp,
Rizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Aizawa,K., Akimura,T., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Hirozane,T., Imotani,K., Ishii,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazume,N., Sasaki,D., Sato,K., Shibata,K.,
Shiraki,T., Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and
Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKEN integrated sequence analysis (RISA) system-384-format
sequencing pipeline with 384 multicapillary sequencer. Genome Res.
10 (11), 1757-1771 (2000)

Computer based methods for the mouse full-length cDNA
encyclopedia real-time sequence clustering for construction of a
nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)

CDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                    295
                                                                                                                                                                                                                                                                                                                                                                                              415
                                                                                                                                                                                                                                                                                                                                                                                                                                                         44;
                                                                                             BF147326 437 bp mRNA linear EST 26-OC uw68h08.y1 Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:3467199 5' similar to TR:054784 054784 DEATH-ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs Nature 420, 563-573 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Laboratory for Genome Exploration Research Group, RIKEN Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-CTel: 81-45-503-9222
Fax: 81-45-503-9216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayatsu,N., Hirozane-Kishikawa,T., Konno,H., Nakamura,M., Sakazume,N., Sato,K., Shiraki,T., Waki,K., Kawai,J., Aizawa,K., Arakawa,T., Fukuda,S., Hara,A., Hashizume,W., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Miyazaki,A., Sakai,K., Sasaki,D., Shibata,K., Shinagawa,A., Yasunishi,A., Yoshino,M., Waterston,R., Lander,E.S., Rogers,J., Birney,E. and Hayashizaki,Y.
KINASE 3 ;, mRNA sequence.
BF147326
BF147326.1 GI:11028721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prepare mouse tissues.

Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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                                                                                                                                                                                                                                                                                                                                                                                              CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
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ilarity 100.0%;
Conservative
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/clone lib="RIKEN full-length enriched, pooled tissues, cell_line=TIB-55B388, etc."
/note="pooled tissues: (sex=mix,cell_line=TIB-55BB88), (sex=mix,cell_line=CRL-1722 L5178Y-R)"
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/mol_type="mRNA"
/db_xref="taxon:10090"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 13;
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hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 428;
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                                                                                                                                  EST 26-OCT-2000
DNA clone
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ORGANISM
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W77571
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415 CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44;
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP);
Tumor Gene Index
                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 439)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                  Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                            Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W77571

439 bp mRNA linear EST 20-JUN-me67e12.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE: 400654 5' similar to PIR: S39269 S39269 DAP-kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1997)
Other ESTs: uw66h08.xl
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                   W77571.1 GI:1387622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human ;, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primer: -40RP from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        quality sequence stop: 402.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="female (lactating)"
/tissue_type="mammary gland"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="IMAGE:3467199"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 44; DB 10; ; Pred. No. 2.8e-10; 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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REFERENCE
AUTHORS
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AA475990
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VERSION
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                                                                                                                                                                         COMMENT
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   415
                                                                                                                                                                                                                         Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 443)

1 (bases 1 to 443)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,

Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,

Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,

Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and

Waterston,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA475990 A43 bp mRNA linear EST 18-JUN-1997 vh25g12.r1 Soares mammary gland NbMMG Mus musculus cDNA clone IMAGE:876550 5' similar to TR:G434847 G434847 DAP-KINASE.;, mRNA
                                                                         Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of MedicineP 4444 Forest Parkway, Box 8501, St. Ld Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further i
MGI:516030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 341.
Location/Qualifiers
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Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL , contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                     The WashU-HHMI Mouse EST Project Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                         AA475990.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mol_type="mRNA"
|strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'clone="IMAGE:400654"
                                                                                                                                                                                                                                                                                                                                                                                                                                         GI:2203841
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Pred. No.
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. 2.8e-10;
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                                                                                                                   Louis,
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                                                                                                                   MO 63108
                         information.
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VERSION
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AA023330
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                                 FEATURES
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JOURNAL
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Best Local
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                   source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wh71b08.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDl clone IMAGE:456375 5' similar to PIR:S39269 S39269 DAP-kinase human ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae (Dases 1 to 446)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuo Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Martanton.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Possible reversed clone: similarity on w. Seq primer: -28m13 rev2 ET from Amersham High quality sequence stop: 228.
                                                                                                                                                                           WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
                                                                                            Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                            Unpublished (1996)
Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleosto
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                             The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCCCCAACATCAT 458
                                                               primer: -28M13 rev2 from Amersham
                                                                                                                                               314 286 1800
314 286 1810
                             quality sequence stop: 406.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/organism="Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="IMAGE:876550"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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Pred. No.
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AI180838
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                                                                                                                                                 FEATURES
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                                                                                                                               source
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Query Match
Best Local Similarity
Matches 44; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 446)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubu Marra,M., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Porest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AI180838
AI180838.1 GI:3731476
                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through
IMAGE Consortium (info@lmage.llnl.gov) for fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The WashU-HHMI Mouse EST Project
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                                                                                                                                                                                                                                                 primer: -28m13 rev2 ET from h quality sequence stop: 432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T 3']; double-stranded cDNA was ligated to Eco RI add (Pharmacia), digested with Not I and cloned into the and Eco RI sites of the modified pTTT3 vector. Librar went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco
1st strand cDNA was primed with a Not I - oligo(dT) pr:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:456375"
                                                                                                                        /mol_type="mRNA"
/strain="C57BL/6J"
/tissue_type="Thymus"
/dev_stage="4 weeks"
                                                    /sex="male"
                                                                              /clone="IMAGE:1395343"
                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="placenta"
/dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'sex="unknown"
                                                                                                      'db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4.0%; Score 44;
00.0%; Pred. No.
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hes 0;
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BF012286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 44; Conserv
      Matches
                                  Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
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      44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index Unpublished (1997) Other ESTS: ux54401.xl Other ESTS: ux54401.xl Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the This Clone is available royalty-free through truther information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 449)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF012286
BF012286.1 GI:10712561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BF012286 449 bp mRNA linear EST 06-OCT-2: ux54a01.yl Soares_NKWMD_mandible Mus musculus cDNA clone IMAGE:3514056 5' similar to TR:043293 043293 ZIP-KINASE.;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 441.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGI:1396936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (house mouse)
                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
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Conservative
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                                                                                                                                                         /lab_host="DH10B"
/(clone_lib="Scares_thymus_2NbMT"
/(clone_lib="Scares_thymus_2NbMT"
/(clone_lib="Scares_thymus_2NbMT"
/(clone_lib="Scares_thymus_2NbMT"
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/(clone_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib="scares_thymus_2ntmod_lib=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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                                  4.0%; Score 44; DB 10; 00.0%; Pred. No. 2.8e-1
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Pred. No.
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      Mismatches
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                                      2.8e-10;
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                                                                     Length 449
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RESULT 39
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AA023742
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Best Local S
Matches 44
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                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                    109 CGCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAGGC 152
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Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Lc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 454)

Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

Materston, R.

Mat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tel: 314 286 1800
Tel: 314 286 1810
Fax: 314 286 1810
Email: mouseestewatson.wustl.edu
Email: mouseestewatson.wustl.edu
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through further information.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seq primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IMAGE Consortium (info@image.llnl.gov)
MGI:274213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA023742.1 GI:1487657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
AA023742
                                                                                                                                                                                               CGCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAGGC 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACATCAT 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCCAACATCAT
                                                                                                                                                                                                                                                                                         Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  quality sequence stop: 450.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone lib="Soares mouse placenta 4NbMP13.5 14.5"
/note=Torgan: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
[5]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digasted with Not I and cloned into the Not I and Eco RI sites of the modified pTTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dev_stage="adult"
lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone="IMAGE: 457325"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                       4.0%;
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                                                                                                                                                                                                                                                                                                                                Score 44; Pred. No.
                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                   DB 9;
                                                                                                                                                                                                                                                                                                                                    2.8e-10;
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                                                                                                                                                                                                                                                                                                                                                                   Length 454;
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DAP-KINASE.
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Dubuque, T.,

Mus.

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ACCESSION
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AA015164
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                                                                                                         DEFINITION
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Best Local Similarity
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.....an ; mRNA sequence.
AA015164
AA015164.1 GJ...
                                                                                                                                                                                                                                                       693 CGCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAGGC 736
                                                                                 AA015164
457 bp mRNA linear EST 31-JUL mi63e06.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:468226 5' similar to PIR:S39269 S39269 DAP-kinase
                                                                                                                                                                                                                                                                                                                   44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contect: Marra M/Mouse EST project
WashU-HHMI Mouse EST project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 456)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu,
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA017794 456 bp mRNA linear EST 21-JAN-1997 mh47g09.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE:445696 5' similar to PIR:S39269 S39269 DAP-kinase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 455.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Waterston, R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human ;, mRNA sequence.
AA017794
AA017794.1 GI:1481180
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                 CGCATTAAGCTCATCGACTTTGGCATCGCGCACAGGATCGAGGC 151
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Soares mouse placenta 4NbMP13:5 14.5"
/note="Organ: placenta; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco
1st strand cDNA was primed with a Not I - oligo(dT) pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="adult"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tissue_type="placenta"
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/clone="IMAGE:445696"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Mus musculus"

mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sex="unknown"
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                                                                                                                                                                                                                                                                                                                                  4.0%;
                                                                                                                                                                                                                                                                                                            Score 44; DB 9; L
Pred. No. 2.8e-10;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      Length 456;
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                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                 ACCESSION
VERSION
KEYWORDS
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AA016932
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Best Local S
Matches 44
                                           ORGANISM
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                                                                                                                                                                AA016932
459 bp mRNA linear BST 21-JAN-19 mh37g08.rl Soares mouse placenta 4NbMP13.5 14.5 Mus musculus cDNA clone IMAGE.444734 5' similar to PIR:S39269 S39269 DAP-kinase -
                                           Mus musculus
                                                                                     EST
                                                                                                    human ; mRNA sequence.
AA016932
AA016932.1 GI:1478564
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. L
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubu, Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 448.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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Fax: 314 286 1810
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Contact: Marra M/Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
                                                             Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Possible reversed clone: similarity
                                                                                                                                                                                                                                                                                                              CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACATCAT 336
                                                                                                                                                                                                                                                                                                                                                      CGCGAGGTGAGCATCCTGCGCGAGATCCGCCAACCATCAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          primer: -28M13 rev2 from Amersham
                                                                                                                                                                                                                                                                                                                                                                                             4.0%; Score 44; DB ilarity 100.0%; Pred. No. 2.8 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
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/clone="IMAGE:468226"
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Rodentia;
  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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3. 2.8e-10;
0;
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AUTHORS
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AA017803
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 284
                                                                                                                                                                                                                                                                                                                         AA017803 mRNA linear mh47a03.rl Soares mouse placenta 4NbMP13.5 14.5 Mus clone IMAGE:445612 5' similar to PIR:S39269 S39269 E
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Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HHMI Mouse EST Project
1 (bases 1 to 465)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                          AA017803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Possible reversed clone: similarity on wrong strand Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: 314 286 1800
Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                           AA017803.1 GI:1481070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGCGAGGTGAGCATCCTGCGCGAGATCCGCCACCCCAACATCAT 458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
ist strand cDNA was primed with a Not I - oligo(dT) primer
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/lab_host="DH10B"
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strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tissue_type="placenta"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone="IMAGE:444734"
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00.0%; Pred. No. 2.8e-
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hes 0;
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musculus cDNA
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AA048970
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Best Local
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                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleo; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinat 1 (bases 1 to 475)

Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dub; Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Schellenberg,K., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA048970 475 bp mRNA linear EST 09-SEP mj50c05.r1 Scares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:479528 5' similar to PIR:S39269 S39269 DAP-kinase
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Fax: 314 286 1810
Washington University School of MedicineP 4444 Forest Park Parkway, Box 8501, St. Ld Tel: 314 286 1800
                                                                  Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                      Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                               human ;, mRNA sequence.
AA048970
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
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                                                                                                                   Unpublished (1996)
                                                                                                                                               The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: -28M13 rev2 from Amersham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      quality sequence stop: 444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M.Fatima Bonaldo."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone lib="Soares mouse placenta 4NbMP13.5 14.5"
/note="Organ: placenta; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site 1: Not I; Site 2: Eco RI;
1st strand cDNA was primed with a Not I - oligo(dT) primer
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/dev_stage="adult"
/lab_host="DH10B"
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/strain="C57BL/6J"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                         GI:1528641
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100.0%; Pred. No. 2.9e-1
ative 0; Mismatches
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hes 0;
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                             Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                  uuj7a01.yl Soares mammary gland NMLMG Mus musculus cDNA clone IMAGE:3374088 5' Similar to TR:Ō54784 O54784 DEATH-ASSOCIATED KINASE 3 ; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 482)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                           Tumor Gene Index
Unpublished (1997)
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This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                    Mus musculus
                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="IMAGE:3374088"
                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
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/mol_type="mRNA"
/strain="C57BL/6J"
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100.0%; Pr
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The WashU-HHMI Mouse EST Project
Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                         MGI:485166
Seq primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Marra M.Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44:
                                                                                                                                                                                                                                                                                                                                                                                                                           Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA467508
AA467508.1 GI:2193648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ve01c12.r1
5' similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 483)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares_mammary_gland_NMLMG"
/note="Vector: p7773D-Pac (Pharmacia) with a modified
polylinker; 1st strand cDNA was prepared from mammary
gland tissue from a lactating female, and was then primed
with a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT7T3 vector. Library is normalized. Library
was constructed by Bento Soares and M. Fatima Bonaldo. "
/mol_type="mRNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tissue_type="mammary gland"
/lab_host="DH10B"
                                                                                                                                           /dev_stage="4 weeks"
/lab_host="DH10B"
                                                                                                                                                                             tissue_type="heart"
                                                                                                                                                                                                     'sex="male"
                                                                                                                                                                                                                          clone="IMAGE:808822"
                                                                                                                                                                                                                                                                                                        organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sex="female (lactating)
                                                                                                                                                                                                                                              db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    483 bp mRNA linear EST 11-JUN Scares mouse NbMH Mus musculus cDNA clone IMAGE:808 to TR:G434847 G434847 DAP-KINASE. ;, mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
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; Pred. No. 2.9e-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.9e-10;
hes 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IMAGE:808822
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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-DB=PUblished_Applications_NA -QFMT=fastap -SUFFIX=rnpb -MINNATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX-blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Database :
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NO MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV MAAP -LARGEQUERY -NEG SCORES=0 -WAIT -LONGLOG -THREADS-1 -XCAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Command_line parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 1/USPTO spool
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seq length: 2000000000
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Ygapop 10.0,
Fgapop 6.0,
Delop 6.0,
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1: /cgn2_6/ptcddata/2/pubpna/US07_PUB

2: /cgn2_6/ptcddata/2/pubpna/US06_NEW

3: /cgn2_6/ptcddata/2/pubpna/US06_NEW
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                                                                                                                            /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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n2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
n2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
n2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
n2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
n2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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n2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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equence 1831, quence 560, Ay quence 17354, equence 10, Ay equence 11, Ay equence 11, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 2, Ay equence 2, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 2, Ay equence 1, Ay equence 1, Ay equence 1, Ay equence 287, Ay equence 287, Ay equence 1918, equence 1918, equence 1918, equence 1918, equence 1918, equence 1918, equence 1918, equence 1918, equence 1918, equence 1918, equence 590, equence 1, App equence 1, App equence 1, App equence 1, App equence 6, App equence 6, App	Sequence Seq	Description

## ALIGNMENTS

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US-10-083-641A-6

US-10-083-641A-6

Sequence 6, Application US/10083641A

Publication No. US20030017568A1

Publication No. US20030017568A1

Publication No. US20030017568A1

Publication No. US20030017568A1

GENERAL INFORMATION:

APPLICANT: HAYSTEAD, TIMOTHY A

TITLE OF INVENTION: SMOOTH MUSCLE MYOSIN PHOSPHATASE ASSOCIATED KINASE

FILE REFERENCE: 1579-647

CURRENT APPLICATION NUMBER: US/10/083,641A

CURRENT APPLICATION NUMBER: 60/271,436

PRIOR FILING DATE: 2001-02-27

NUMBER OF SEQ ID NOS: 17

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 6

LENGTH: 1093

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Putative nucleotide

FEATURE:

FEATURE:
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Result

% Query

SUMMARIES

318 903

338 963

1023

1083 358

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Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Alignment Scores: Pred. No.: Score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; NAME/KEY: Unsure
; LOCATION: (2), (7), (
; OTHER INFORMATION: N
US-10-083-641A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (1-361) x US-10-083-641A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CysArgAlaSerValLeuSerLeuLysAlaIleProLysCysLeuSer****GlySerLeu
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LeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrThrTrpLeuGly
                                                                                                 ArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyLeuThrCys
                                                                                                                                                                ACAGGATCGAGGCCGGTAGCGAGTTCAAGAACATCTTTGGCACGCCAGAGTTCGTCGGTG
                                                                                                                                                                                          ThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGlnSerSerSerVal
                                                                                                                                                                                                                                                   TGTTGCTGGACAAGCATGCAGCCAGCCCACGCATTAAGCTCATCGACTTTGGCATCGCGC
                                                                                                                                                                                                                                                                                  CysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuAlaSerArg
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AlaGluLysAspHis***GlnArqMetArqProArqSerSerSerSerArqSerTrpThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGCGAACTTTTCGACTTTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGlyGluLeuPheAspPheLeu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGCATCCTGCGCGAGATCCGCCACCCCAACATCATCACGCTGCACGATGTTGTTCGAGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArgGluVal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPheIleLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LeuProSerSerGlySerAlaAlaLeuSerCysSerPheProHisSerGly----PheAla
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                                                                                                                                                                                                                                                                                                                                              GTGTCCACTACCTGCACTCCAAGCGCATCGCGCACTTTGACCTGAAGCCGGGAGAACATCA
                                                                                                                                                                                                                                                                                                                                                                                  ValSerThrThrCysThrProSerAlaSerArgThrLeuThr***SerArgArgThrSer
                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTGAGAAGGATCACTGACAGAGGATGAGGCCACGCAGTTCCTCAAGCAGATCCTGGACG
                                                                       AGGGGCAGGTGTGGGCACCACCCGATAGGGTAGATTTTGCACGGCCTTGGCCTGACCTGC
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be A, C, G or (
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APPLICANT: ZIONG, MGI
TITLE OF INVENTION: NOVEL HUMAN PROTEINS, POLYNUCLEOTIDES ENCODING THEM AND
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 21402-462D
CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/327,454
PRIOR APPLICATION NUMBER: 60/327,917
PRIOR FILING DATE: 2001-10-05
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/328,029
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR APPLICATION NUMBER: 60/328,056
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR APPLICATION NUMBER: 60/329,414
PRIOR APPLICATION NUMBER: 60/341,058
PRIOR APPLICATION NUMBER: 60/341,058
PRIOR APPLICATION NUMBER: 60/341,058
PRIOR APPLICATION NUMBER: 60/343,629
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-24
PRIOR FILING DATE: 2001-10-29
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PRIOR FILING DATE: 20
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US-10-262-445-118
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Publication No. US20040014058A1
GENERAL INFORMATION:
APPLICANT: Alsobrook II, John
APPLICANT: Burgess, Catherine
APPLICANT: Catterton, Elina
  Remaining Prior Application da
NUMBER OF SEQ ID NOS: 133
SOFTWARE: CuraSeqList version
SEQ ID NO 118
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Patturajan, Meera
Rieger, Daniel
Spytek, Kimberly
Taupier Jr., Raymond J
Zerhusen, Bryan
Zhong, Haihong
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Chaudhuri, A...
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Mezes, Peter
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da, Ramesh
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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; LOCATION: (94)..(1455)
US-10-262-445-118
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ORGANISM: Homo:
FEATURE:
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 817 AGCAA-----CACCAG 827
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                               351 spMetProGlyProHisGln 357
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                                                               GAGACGCTCAC----CAACATCTCAGCCGTGAACTACGACTTCGACGAGGAGTACTTC
                                                                                            lyThrSerAlaAsnCysLysHisTrpGly***GluMetSerLeu-----GlyThrLeuA 351
                                                                                                                                                           spGlyGlnGlyProGln-----ThrValProAlaArgGlyProGlyIleArgAlaG
                                                                                                                                                                                                                                                                                             euThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrThrT 296
                                                                                                                                                                                                                                                                                                                                                              rSerVal-ArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyL 276
                                                                                                                                                                                                                                                                                                                                                                                                   aSerArgThrGlySerArgProValAlaSerSerArgThrSerLeuAlaArgGlnSerSe 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACATCATGCTGCTGGACAAGAACGTGCCCAACCCACGAATCAAGCTCATCGACTTCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gThrSerCysCysTrpThrSerMetGlnProAlaHisAlaLeuSerSerSerThrLeuAl 236
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                                                                                                                                                                                                                                                                                                                                  TTCGGCACCCCGGAGTTTGTGGC------
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RESULT 4
US-10-087-192-1835
US-10-087-192-1835
Sequence 1835, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: MORY'S, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER
FILE REFERENCE: 529452000122
CCURRENT APPLICATION NUMBER: US/10/087,192
CCURRENT APPLICATION NUMBER: US/10/087,192
CCURRENT APPLICATION NUMBER: US/747,377
PRIOR APPLICATION NUMBER: US/9/747,377
PRIOR APPLICATION NUMBER: US/9/798,586
PRIOR APPLICATION NUMBER: US/9/798,586
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PRIOR APPLICATION NUMBER: US/9/798,586
PRIOR APPLICATION NUMBER: US/9/798,586
PRIOR APPLICATION NUMBER: US/9/798,586
PRIOR APPLICATION NUMBER: US/9/798,586
PRIOR APPLICATION FILLING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOCTWARE: FSSK-SEQ for Windows Version 4.0
PUBBER DNS: LENGTH: 1716
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; ORGANISM: Homo
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APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Van 't Veer, Laura Johanna
APPLICANT: Bernards, Rene
ITITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 9301-188-999
CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: 60/298,918
PRIOR FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/298,710
PRIOR APPLICATION NUMBER: 60/380,710
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
VUMBER OF SEQ ID NOS: 2699
LENGTH: 5910
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-342-887-1105
                                         Percent Similarity:
Best Local Similarit;
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DB:
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Publication No. US20040058340A1
GENERAL INFORMATION:
APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
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Mao, Mao
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TITLE OF INVENTION: DAP-Kinase and HOXA9, Two Human Genes Associated with Genesis, TITLE OF INVENTION: Progression, and Aggressiveness of Non-Small Cell Lung Cancer FILE REFERENCE: 10620-111 CURRENT APPLICATION NUMBER: US/10/045,400C CURRENT FILING DATE: 2001-11-29 PRIOR APPLICATION NUMBER: US 60/250,083 PRIOR FILING DATE: 2000-11-29 SOFTWARE: PatentIn version 3.1 SEQ ID NO 4

LENGTH: 5910

TYPE- NUMBER: 5910
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/10045400C Publication No. US20030224509A1 GENERAL INFORMATION:
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                                                                      APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Nan', Chris
APPLICANT: Van't Veer, Laura
APPLICANT: Van't Veer, Marc
APPLICANT: Van't Veer, Marc
APPLICANT: Van't Sene
TITLE OF INVENTION: Diagnosis and Prognosis of
FILE REFERENCE: 3901-175-999
CURRENT APPLICATION NUMBER: US/10/172,118
CCURRENT FILING DATE: 2002-06-14
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US-10-172-118-1105
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Query Match:
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PRIOR APPLICATION NUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1105
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RESULT 6 US-10-045-400C-4

APPLICANT: Moon, Chu APPLICANT: Mao, Li

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FEATURE: CDS
NAME/KEY: CDS
LOCATION: (337)...(4632)
OTHER INFORMATION:
US-10-045-400C-4

LENGTH: 5910 TYPE: DNA ORGANISM: Homo sapiens

Alignment Scores: Pred. No.:

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; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: NM
; DATABASE ENTRY DATE: 2001-06-7
US-10-172-118-1105
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Sequence 12, Application US/10133937

Publication No. US20030207278A1

GENERAL INFORMATION:

APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
APPLICANT: Meterson, Carsten
APPLICANT: Meltzer, Paul
TITLE OF INVENTION: METHODS FOR ANALYZING HIGH DIMENSIONAL DATA FOR CLASSIFYING,
TITLE OF INVENTION: DIAGNOSING, PROGNOSTICATING, AND/OR PREDICTING DISEASES AND
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Best Local Similarity
Query Match:
DB:
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FILE REFERENCE: 11613.55USO1
; CURRENT APPLICATION NUMBER: US/10/133,937
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 12
; LENGTH: 5910
; TYPE: DNA
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; ORGANISM: Homo
US-10-133-937-12
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 Sequence 37, Application US/10352684A Publication No. US20030215452A1 GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals APPLICANT: Carroll, Joseph M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                No.:
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APPLICANT: Healy, Alleen
APPLICANT: Weich, Madine S.
APPLICANT: Weich, Madine S.
APPLICANT: Weich, METHODS AND COMPOSITIONS FOR TREATING
TITLE OF INVENTION: HEMATOLOGICAL DISCORDERS USING 131, 148, 199, 12303, 13906,
TITLE OF INVENTION: HEMATOLOGICAL DISCORDERS USING 131, 148, 199, 12303, 13906,
TITLE OF INVENTION: 15513, 17822, 302, 5577, 194, 14933, 28059, 7366, 12212,
TITLE OF INVENTION: 1591, 261, 12416, 270, 1410, 137, 1871, 13051, 1849,
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
CURRENT FAPLICATION NUMBER: US 60/354, 333
PRIOR FILING DATE: 2002-00-128
PRIOR APPLICATION NUMBER: US 60/354, 333
PRIOR FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US 60/364, 476
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/354, 476
PRIOR FILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: US 60/396, 494
PRIOR FILING DATE: 2002-06-06
PRIOR FILING DATE: 2002-06-06-24
PRIOR APPLICATION NUMBER: US 60/396, 494
PRIOR APPLICATION NUMBER: US 60/396, 494
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; NAME/KEY: CDS
; LOCATION: (337)...(4632)
US-10-352-684A-37
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SOFTMARE: FastSEQ for Windows Version 4.0
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ORGANISM: Homo Sapiens
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                                           PheLeuAlaGluLysAspHis***Gln-ArgMetArgProArgSerSerSerSerArgSe
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; TYPE: DNA
; ORGANISM: Homo sapiens
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APPLICANT: Hevezi, receir.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and TITLE OF INVENTION: Methods of Screening for Modulators of Cancer FILE REFERENCE: 018801-012500US
FILE REFERENCE: 018801-012500US
CURRENT FILING DATE: 2000-01-13
PRIOR APPLICATION NUMBER: US/10/295,027
CURRENT FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-01-08
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/347,349
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PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,714
Remaining Prior Application
NUMBER OF SEQ ID NOS: 1386
SOFTWARB: Patentin Ver. 2:
SEQ ID NO 1018
LENGTH: 5910
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                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/356,714 PRIOR FILING DATE: 2002-02-13
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Gish, Kurt C.
Glynne, Richard
Hevezi, Peter A.
Mack, David H.
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CURRENT APPLICATION NUMBER: US/10/159,563
CURRENT FILING DATE: 2002-12-09
PRIOR APPLICATION NUMBER: US 10/133,937
PRIOR FILING DATE: 2002-04-25
NUMBER OF SEQ ID NOS: 444
SOFTWARE: PATENTIAL TOWNS AND THE SEQ ID NOS: 444
SOFTWARE: PATENTIAL VERSION 3.1
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Publication No. US20040009154A1
GENERAL INFORMATION:
APPLICANT: Khan, Javed
APPLICANT: Ringner, Markus
APPLICANT: Peterson, Carsten
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                                                                                 ; Sequence 4, Application US/10303588
; Publication No. US20040116364A1
; GENERAL INFORMATION:
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: MODULATION OF DEATH-ASSC;
; FILE REFERENCE: HTS-0071
; CURRENT APPLICATION UMBER: US/10/303,588
; CURRENT FILING DATE: 2002-11-22
; NUMBER OF SEQ ID NOS: 78
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RESULT 13
US-09-9711-392-65
(Sequence 65, Application US/09971392
Publication No. US20030134283A1
(GENERAL INFORMATION:
APPLICANT: Peterson, David P.
APPLICANT: Pearson, Cecelia I.
APPLICANT: Cocks, Benjamin G.
FILE REFERENCE: PA-0029 US
FILE REFERENCE: PA-0029 US
CURRENT APPLICATION NUMBER: US/09/971,392
CURRENT FILING DATE: 2001-10-03
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Best Local Similarity:
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FEATURE:
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NAME/KEY: CDS
LOCATION: (337)...
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Templ
US-09-971-392-65
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PRIOR FILING DATE: 2000-10-03
NUMBER OF SEQ ID NOS: 260
SOFTWARE: PERL Program
SEQ ID NO 65
LENGTH: 6046
TYPE: DNA
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pLeuGlySer***TyrValGluHisArgArgHisHisLeuHisPro
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                                                   AACATATTTGGG-ACTCCAGAGTTTGTCGCTCCTGA-GATAGTCAACTATGAACCTCTTG
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RESULT 14
US-10-252-157-452
; Sequence 452, Application US/10252157
; Publication No. US20030190640A1
; GENERAL INFORMATION:
; APPLICANT: Faris, Mary

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030190640A1 900031.4
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RESULT 15
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CURRENT FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: 60/295,048
PRIOR FILING DATE: 2001-05-31
NUMBER OF SEQ ID NOS: 501
SOFTWARE: PERL Program
SEQ ID NO 452.
LENGTH: 6046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Pearson, Cecelia I.
TITLE OF INVENTION: GENES EXPRESSED IN PROSTATE CANCER
FILE REFERENCE: PA-0027-1 US
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                                                       pLeuGlySer***TyrValGluHisArgArgHisHisLeuHisPro 311
                                                                                     rSerValArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyLe
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Matches:
Conservative:

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Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morris, David W.
APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS
TITLE OF INVENTION: CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1832
LENGTH: 1592
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ORGANISM: Mus
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Result
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-MODBL=frame+ pin.model -DEV=xlh
-Q-(cgn2 1)(USPTO_Spool/GBEREYESUS641/runat_29062004_143150_24548/app_query.fasta_1.519
-DB=N_Geneseq_29Jan04 -QFMT=fastap -SUFFIX=rng -MINNATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bite -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=20000000
-USER-GEBREYESUS641 @CGN 1 1_470 @runat 29062004 143150_24548 -NCFU=6 -ICFU=3
-NO_MMAP -LARGEQUERY -NEG_SCORE=0 -MAIT -DSPBLOCK=100 -LONGLOG
-NORMAP -LARGEQUERY -NEG_SCORE=0 -MAIT -DSPBLOCK=100 -LONGLOG
-NORMAP -LARGEQUERY -NEG_SCORE=0 -MAIT -DSPBLOCK=100 -LONGLOG
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-NORMAP -LARGEQUERY -NEG_SCORE=0 -MAIT -DSPBLOCK=100 -LONGLOG
-NEG TIMBOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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myosin light chain phosphatase; smooth muscle disease;
c; hypotensive; muscular; hypertension.
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P-PSDB; ABG70856.
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                                                                     LeuProSerSerGlySerAlaAlaLeuSerCysSerPheProHisSerGly---PheAla
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Toxicity-related gene, SEQ ID 3489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where compound, predicting to a database comprising SEQ ID 1-4925, where compound, predicting hepatotoxicity or the progression of a toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or compound modulates in a cell, and identifying an agent that modulates the consect or compound modulates in a cell, and identifying an agent that modulates at compound modulates in a cell, and identifying an agent that modulates at compound modulates in a cell, and identifying an agent that modulates at cleast one activity of a protein. The method and compositions of the present invention using a database of genes having liver toxin-induced differential expression, are useful in identifying toxicity markers in cliver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the princed compositions of the compositions of the compositions of the compositions of the compositions of the compositions of the compositions of the compositions of the compositions of the compositions of the compositions of the compositions 
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15-MAR-2002;
30-DEC-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1514 BP;
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                          rTrpThrValSerThrThrCysThrProSerAlaSerArgThrLeuThr****SerArgAr
                                                                                                   PheLeuAlaGluLysAsp-His***GlnArgMetArgProArgSerSerSerSerArgSe
                                                                                                                                                               GAGAACAAGACAGATGTGGTGCTGATCTTGGAGCTGGTGTCCGGCGGAACTTTTCGAC
                                                                                                                                                                                            GluAsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAsp
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  CTGGACGGTGTCCACTACCTGCACTCCAAGCGCATCGCGCACTTTGACCTGAAGCCGGAG
                                                                                  TTTCTGGCTGAGAAGGAGTCACTGACAGAGGATGAGGCCA
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04-SEP-2002;
28-JAN-2003;
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11-APR-2002;
19-APR-2002;
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13-MAR-2002;
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                    LOGIC INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Determining if a compound induces a toxic effect on a tissue or cell, for identifying hepatotoxic compounds, comprises comparing a gene expression profile of a tissue or cell sample to a database of Tox mean and non-Tox
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                              rSerValArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyLe
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                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
FIGURE9 (1-361) x AAX34657 (1-1429)
                                                                                                                                                                                            Alignment
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                                                                                                                                                                                                                                                                                                         The invention provides human and murine recombinant Zipper Interacting protein Kinase (ZIP-kinase) proteins. These proteins are serine/threonine kinases which bind the leucine zipper domain of transcription factor ATF4. Host cells containing vectors comprising the ZIP-kinase nucleic acids are used for the recombinant expression of the proteins. ZIP-kinase protein and DNA are useful as gene therapeutic agents against cancer, and as anti-cancer agents. The present sequence represents a DNA encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Recombinant Zipper Interacting and DNA, useful as anticancer agent
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leucine zipper domain; transcription factor ATF4; gene therapy; cancer;
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murine ZIP kinase
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Ota T, Nishikawa T,
Wakamatsu A, Sugiya
                                                                     (HELI-) HELIX RES INST
2001~524255/58.
DB; AAM93338.
                                Sugiyama
                                Isogai T,
a T, Nagai
                                Hayashi K,
K, Kojima
                                Ishii S,
S, Otsuki
                                Kawai Y;
T, Koga
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830 Primers useful for synthesizing in genetic manipulation. full length cDNA clones and their use

8 SEQ ID NO 2874; 1380pp + Sequence Listing; English

The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nuclectide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is a full length human cDNA of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly

Sequence 2079 ₽P; 396 A; 626 ç 733 ດ 324 Η. 0 Ç 0 Other;

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Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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rSerVal-ArgGlyArgCysGlyHisHisProIleGly***IleLeuHisGlyLeuGlyL
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                  The present sequence encodes human DAPK3. The expression level of the gene is used in the method of the invention. The specification describes a method of examining chronic myelogenous leukemia. The method comprises measuring the expression level of a gene selected from IFIT-2, LAGE-1, BAGE, DDB1, ETS2. PIASy, PIASx-alpha, PIASx-beta and DAPK3, or determining the expression profile of a group of genes including one or more of these genes, in a cell or tissue sample from a chronic myelogenous leukemia patient. The method is used for the diagnosis, treatment and prevention of chronic myelogenous leukemia patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human;
PIASy;
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P-PSDB;
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PIASX-alpha; PIASX-beta; DAPK3; gene; ss.
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Best Local Similarity:
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S, Millet I,
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                                                                        The invention relates to a novel method for diagnosing a cancer in a complete, the method comprises determining, in a sample from the subject, the level of at least one polypeptide, where a higher level of the compared to the level of the polypeptide in a subject free of concer is indicative of cancer. The polypeptide is selected from any of the polypeptides encoded by the polynucleotides listed in the specification and polypeptides which are at least 70% homologous to the polypeptides. The method of the invention has cytostatic activity, and may have a use in gene therapy. The method is useful in identifying markers specific for one or several types of cancer, depending on the tissue origin, which may be used in numerous diagnostic and prognostic applications as well as cancer type-specific the acreets for therapeutic contervention. The compounds that modulate the activity of a tumour suppressor gene are useful in the treatment of cancer or as anti-cancer suppressor gene are useful in the treatment of cancer or as anti-cancer.
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                                                       sequence represents a polynucleotide of
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Alignment Scores: Pred. No.:

Sequence 2226

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0 **G** 

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Length: Matches:

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              CDNA
                                                                                        standard;
                                                                                                                                                               spMetProGlyProHisGln
                                                                                                                                                                                        GAGACGCTCAC
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                                                                                                                                                                                                                                                                                        GGCCTGGAGGCATGTGGAGCATCGGTGTCATCACCTATATCCT
                                                                                                                                                                                                                                                                                                                                                                euThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrThrT
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57.84%
34.61%
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            SEQ ID
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            NO:14925
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46
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27-AUG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-00241899.
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Sugiyama
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                                                                                                                                                                                                                                                       detection; diagnosis; antisense therapy; gene therapy;
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T, Wakama
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Wakamatsu
                                                                                                                                                              Hayashi K,
A, Nagai K,
                                                                                                                                                               Saito K,
C, Otsuki
                                                                                                                                                               Yamamoto
T;
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Primer sets for synthesizing polynucleotides, particularly the 56 length cDNAs defined in the specification, and for the detection diagnosis of the abnormality of the proteins encoded by the fullrly the 5602 full-detection and/or the full-length

Claim 8; SEQ ID NO 14925; 2537pp + Sequence Listing; English

CC Inagth cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC coligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprises a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC oplynucleotide which comprises a 3'-end sequence complementary to a
CC oligonucleotide which comprises a 3'-end sequence of the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC cDNAs easily without any specialised methods. AAH33166 to AAH33628 and
CC cDNAs easily without any specialised methods. AAH33165 to AAH3363 represent
CC cDNAs easily without any specialised methods. AAH33165 to AAH3363 represent
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419 A 929 Ç ē 343 Η. 0 ₽. 0 Other;

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Best Local Similarity:
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                                                                                   (1-361) x AAH16158
344
                   117
                IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg
                                       TTTGCGATCGTGCGGAAGTGCCGGCAGAAGGGCACGGGCAAGGAGTACGCAAGTTC
                                                           PheAlaIleValArgLysCys---
                                                                                                       8.896
631.50
69.128
65.4128
4.5588
                                                                                   (1-2224)
                                                                                                               Conservative:
Mismatches:
Indels:
                                                     ---LysGlyThrGlyMetGluTyrAlaAlaLysPhe
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Matches:
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RESULT 11
AAAT78068
ID 7AAAT78
XX AAH78
AC AAH78
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C, Otsuki
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                        Yamamoto T, Funah
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rpLeuGlySer***TyrValGluHisArgArgHisHisLeuHisPro
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EPO
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11-JAN-2000; 2000JP-00118774.
02-MAY-2000; 2000JP-00183765.
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su A, Sugiyama
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GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
                                                   ATCAAGAAGCGCCCGCCTGTCATCCAGCCGGCGTGGGGTGAGCCGGGAGGAGATCGAGCGG
                                                                                            IleLysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArg
                                                                                                                                                                                         PheAlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPhe
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a T, Nagai
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K, Kojima
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S, Otsuki
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T, Koga
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02-MAY-2000; 2000JP-00183765
                                                                                                                                                                                                                                                                                             Human;
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          830 Primers useful for synthesizing full length cDNA clones and their use in genetic manipulation.
                                                                           Wakamatsu
                                                                                      Ota T,
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                                                                        Nishikawa T, isu A, Sugiyama
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                                                                        Isogai T,
a T, Nagai
                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 316
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                                                                         Hayashi K,
K, Kojima
                                                                        Ishii S,
S, Otsuki
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                                                                        Kawai Y;
T, Koga
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Claim

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The invention relates to primers for synthesising full length cDNA clones. 830 cDNA molecules encoding a human protein have been isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA molecules have been determined. Primers for synthesising the full length cDNA are useful for clarifying the function of the protein encoded by the cDNA. The full length clones were obtained by construction of full length enriched cDNA libraries that were synthesised by the oligo-capping method. The primers enable the production of the full length cDNA easily without any special methods. The present sequence is the nucleotide sequence of the 5'-end of a cDNA provided in the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in CD-ROM format directly from EPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GluValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPhe
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                                                                           pLeuGlySer***TyrValGluHis-ArgArgHisHisLeuHisProValSerAla***A
                                                                                                                                                                                                                                                         ATCGCNCACAAGATCGANGCGGGGAACGAATTCAANAACATCTTCGGCACCCCGGAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TICCTGGGGAGAAGGAGTCGCTGACGGAGGAAGCCACCCAGTTCCTCAAGCAGATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PheLeuAlaGluLysAspHis***-GlnArgMetArgProArgSerSerSerSerArgSe
                                                                                                                                                  uThrCysLeuAsnAsnProValPheHisSerPro***AspCysLysLeu***ThrThrTr
                                                                                                                                                                                   TGTGGCCCCANAAATTGTGAACTATGAACCGCTGGGC------
                                                                                                                                                                                                                    rSerValArgGlyArgCysGlyHisHisProlleGly***IleLeuHisGlyLeuGlyLe
                                                                                                                                                                                                                                                                                                                                                                                              CTGGACGGCGTTCACTACCTGCACTCTAAGCGCATCGCACACTTTGACCTGAAGCCGGAA
                                               -CTTGGAAGCNGACATGTTGAACATCCGT
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Mismatches:
Indels:
Gaps:
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28-JUN-2000;
30-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
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26-JUL-2000;
14-AUG-2000;
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2000US-0224518P

2000US-0224518P

2000US-0224519P

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spGlyGlnGlyPro

656 296 Percent Similarity:
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Query Match:
DB:

2.67e-26 581.50 66.37% 59.73% 31.85%

FIGURE9

(1-361)

x AAK91856 (1-757)

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199 117 Alignment Scores: Pred. No.:

757

BP;

176 A; 219 C;

220

antigen; SEQ

ID NO:25453. cancer;

2000US-0232081P

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Percent Similarity:
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Score:
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AsnLysThrAspValValLeuIleLeuGluLeuValSerGlyGlyGluLeuPheAspPhe
                                             GTGAACATCCTGCGGGAGATCCGGCACCCCAACATCATCACCCTGCACGACATCTTCGAG
                                                            ValSerIleLeuArgGluIleArgHisProAsnIleIleThrLeuHisAspValPheGlu
                                                                                                                        LysLysArgArgLeuProSerSerArgArgGlyValSerArgGluGluIleGluArgGlu
                                                                                                                                                               AlaIleValArgLysCys-----LysGlyThrGlyMetGluTyrAlaAlaLysPheIle
                                                                                                       AAGAAGCGCCGCCTGTCATCCAGCCGGCGTGGGGTGAGCCGGGAGGAGCATCGAGCGGGAG
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2000US-0251866P.
2000US-0251869P.
2000US-0251869P.
2000US-0251989P.
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RESULT 15
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CC sequences. (1) is useful as hybridisation probes, polymerase chain of reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed compared to the sequence tags for identifying expressed compared to the sequence tags for identifying expressed compared to the sequence tags for identifying expressed compared to the sequence tags for identifying expressed compared to the sequence tags for identifying expressed compared to the sequence of the sequence of the sequence of the sequence of the sequence have applicated in the sequence of sites expressing (II). (I) and (II) are useful for treating disorders of the sequence have applications in consists. The composition of the sequence have applications in consists of the sequence of the statist to assess biodiversity cresponsible for genetic disorders or other traits to assess biodiversity conditions and sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this content did not appear in the printed specification, but was obtained in cettp-wipo.int/pub/published\_pct\_sequences. New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess Claim 1; SEQ ID NO 9265; 103pp; English. polynucleotide (I) and polypeptide

(II)

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